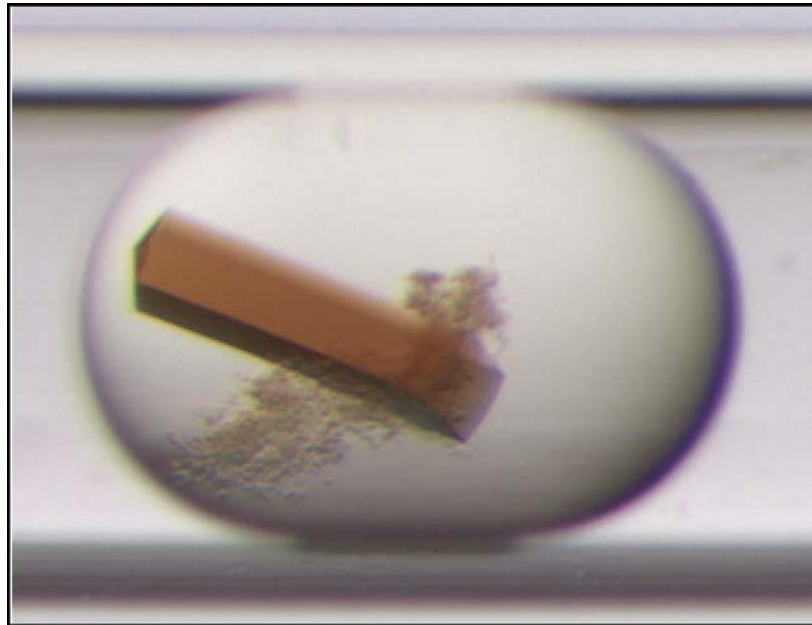


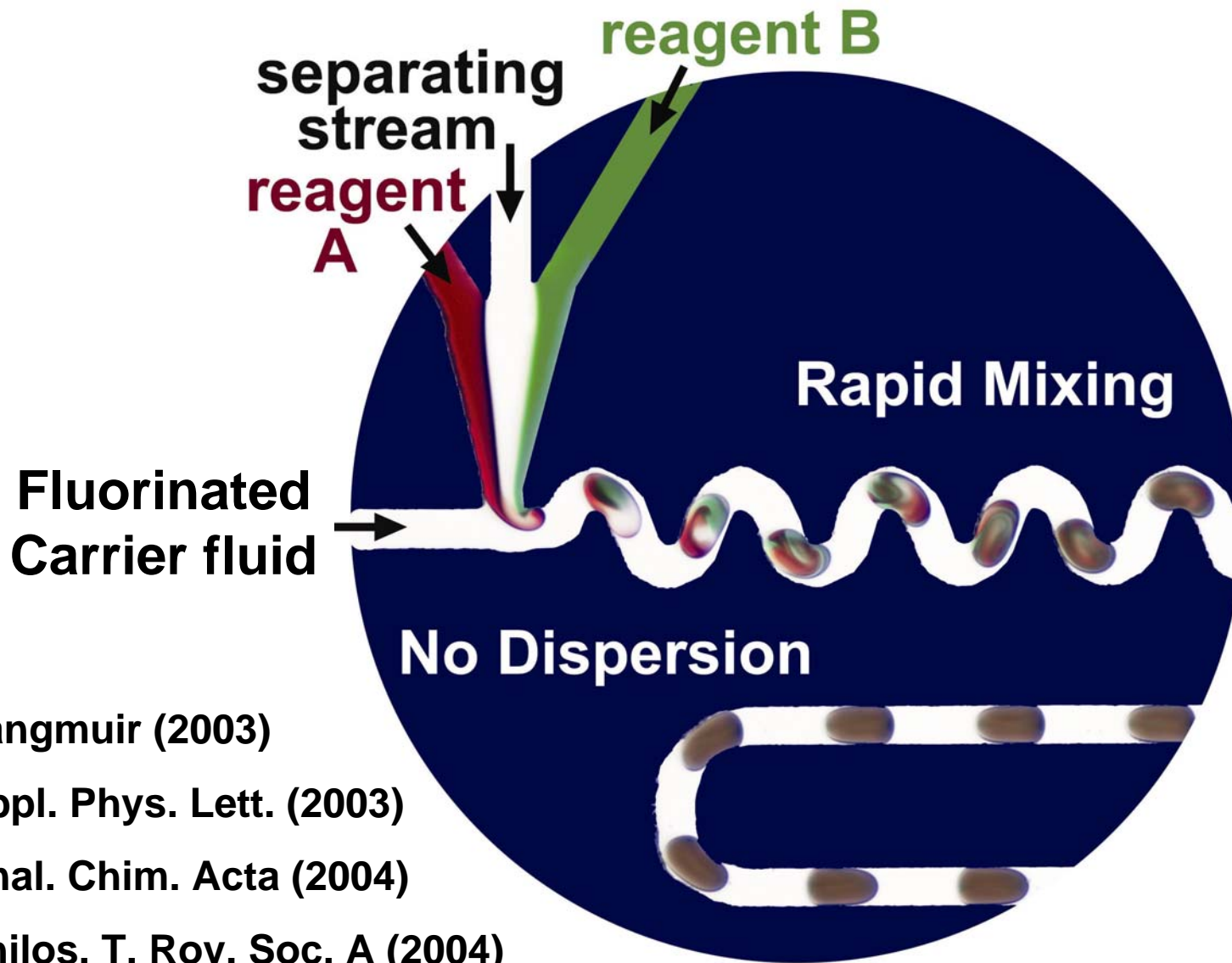
Crystallization of Membrane Proteins in Nanoliter Volumes Using Plug-based Microfluidics



**Liang Li, Cory Gerdt, Debarshi Mustafi, Qiang Fu, Delai Chen
Rustem Ismagilov***

**The University of Chicago
June 20th, 2007**

Formation of Droplets (Plugs) in Microfluidics



Langmuir (2003)

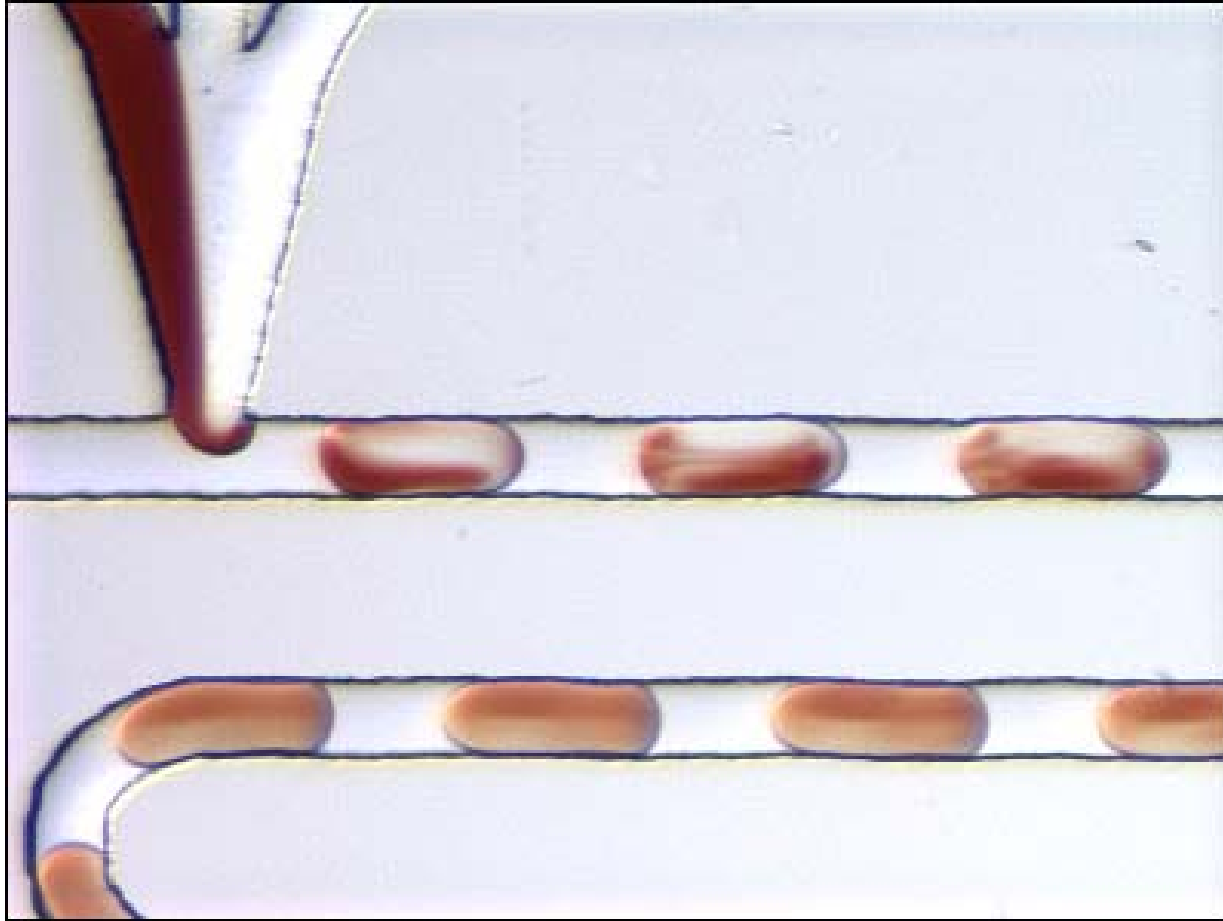
Appl. Phys. Lett. (2003)

Anal. Chim. Acta (2004)

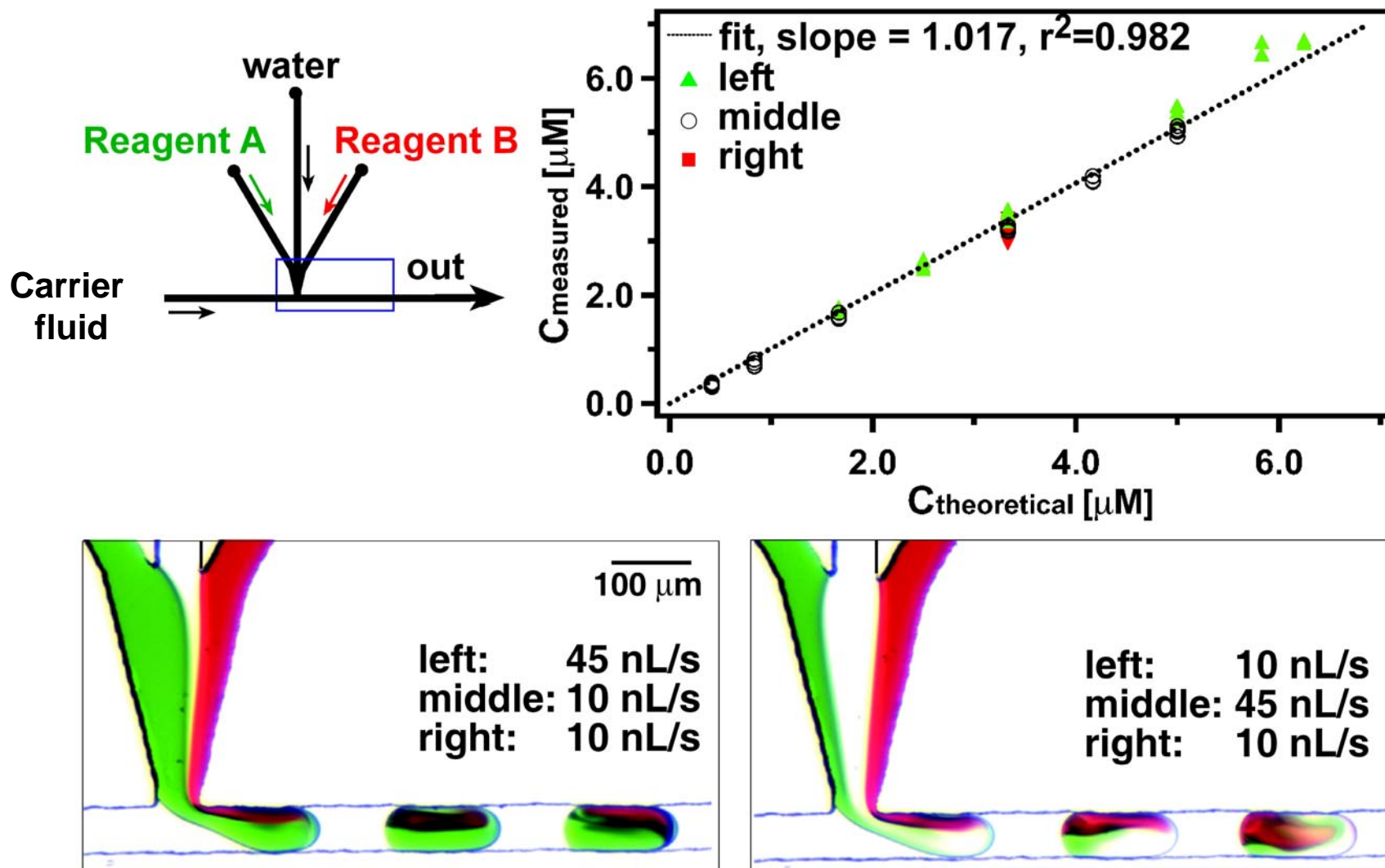
Philos. T. Roy. Soc. A (2004)

H. Song, J. D. Tice, R. F. Ismagilov *Angew. Chem.-Int. Edit.* 2003, 42, 768.

Eliminate Dispersion: Plugs Form in Fluorinated Carrier Fluid

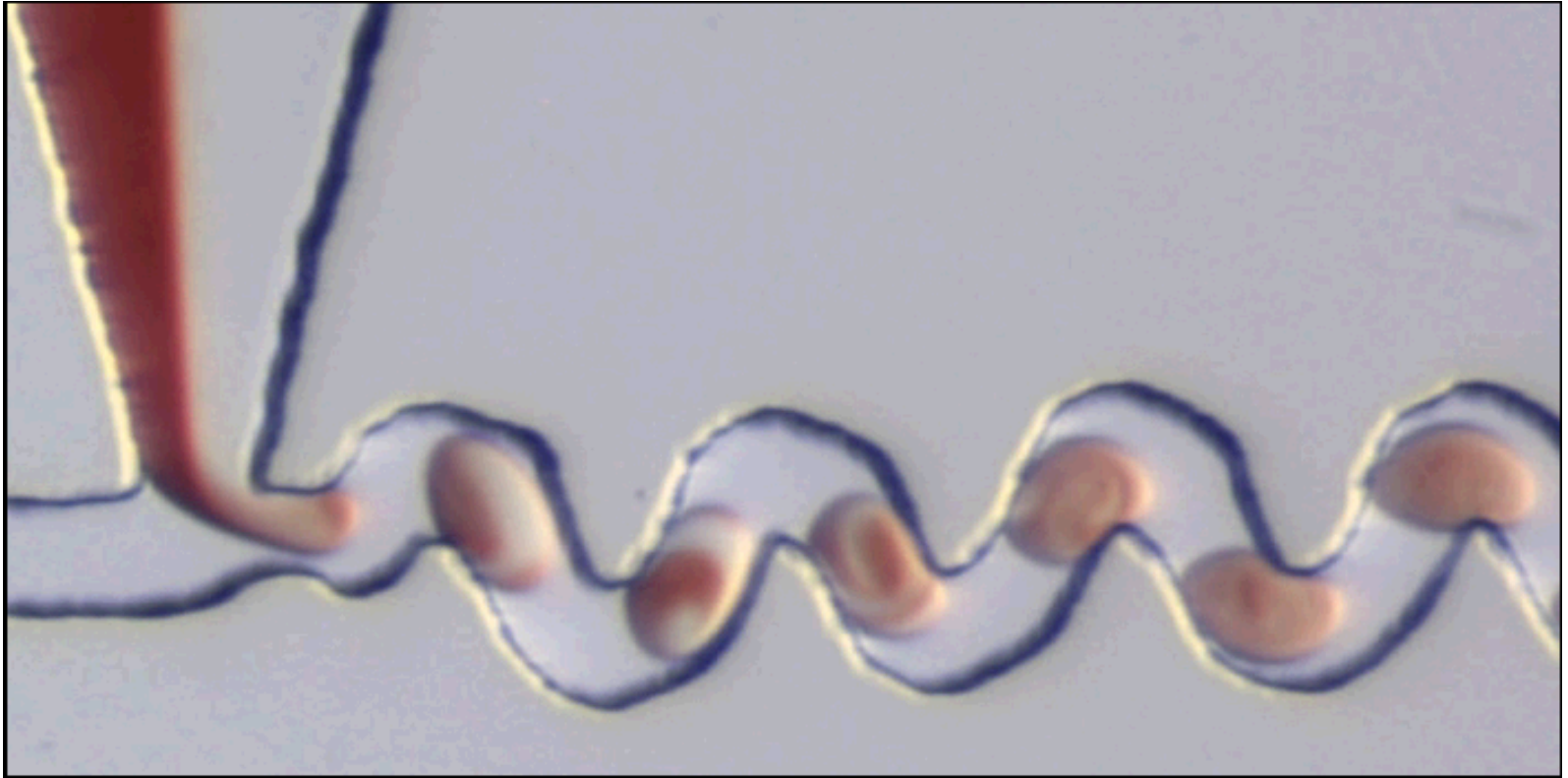


Control Concentrations: Vary the Flow Rates

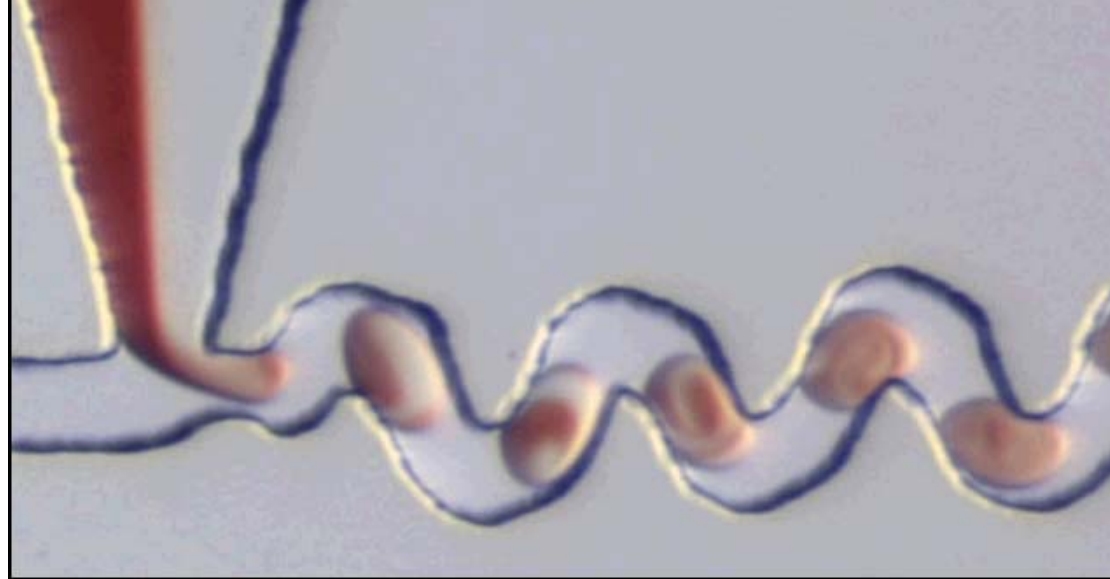
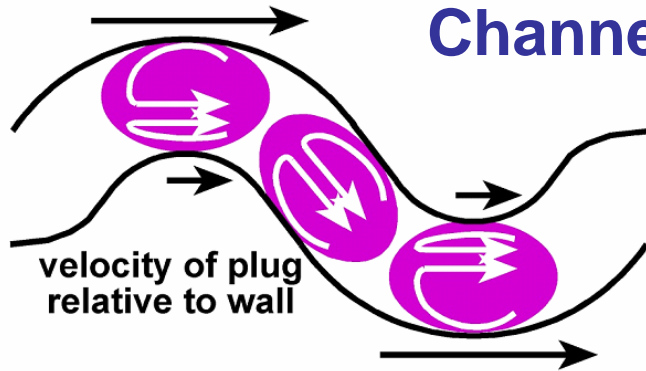


H. Song and R. F. Ismagilov *J. Am. Chem. Soc.* 2003, 125, 14613.

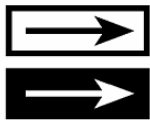
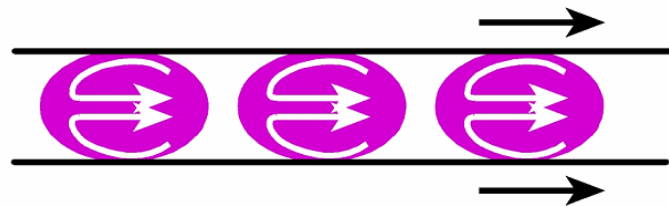
Enhance Mixing Rate: Use Winding Channels



Rapid Mixing in Winding Channels

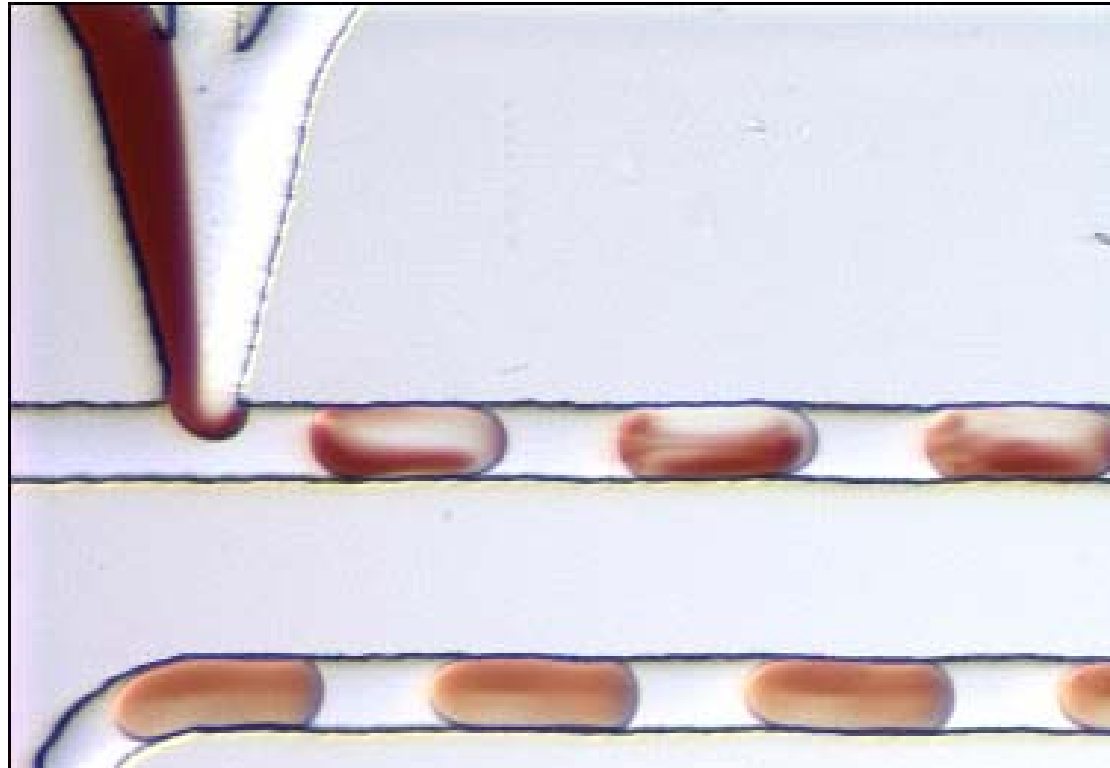


Slow Mixing in Straight Channels

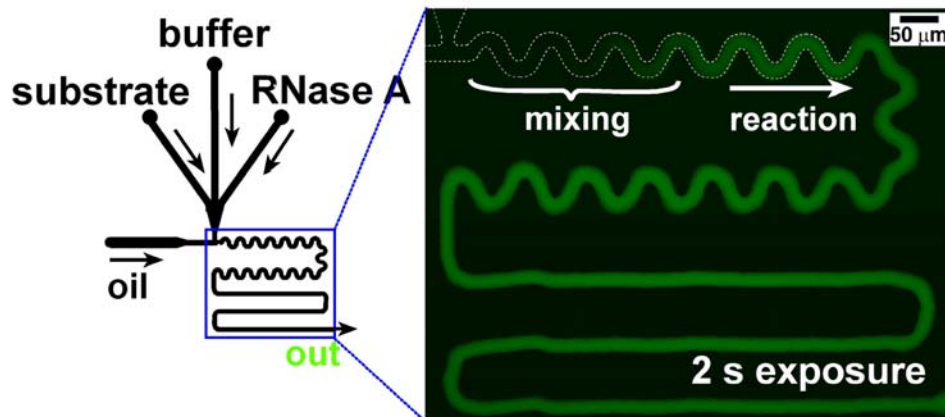


velocity of plug relative to wall

flow within plugs



Millisecond Kinetics Using Nanoliters of Solution

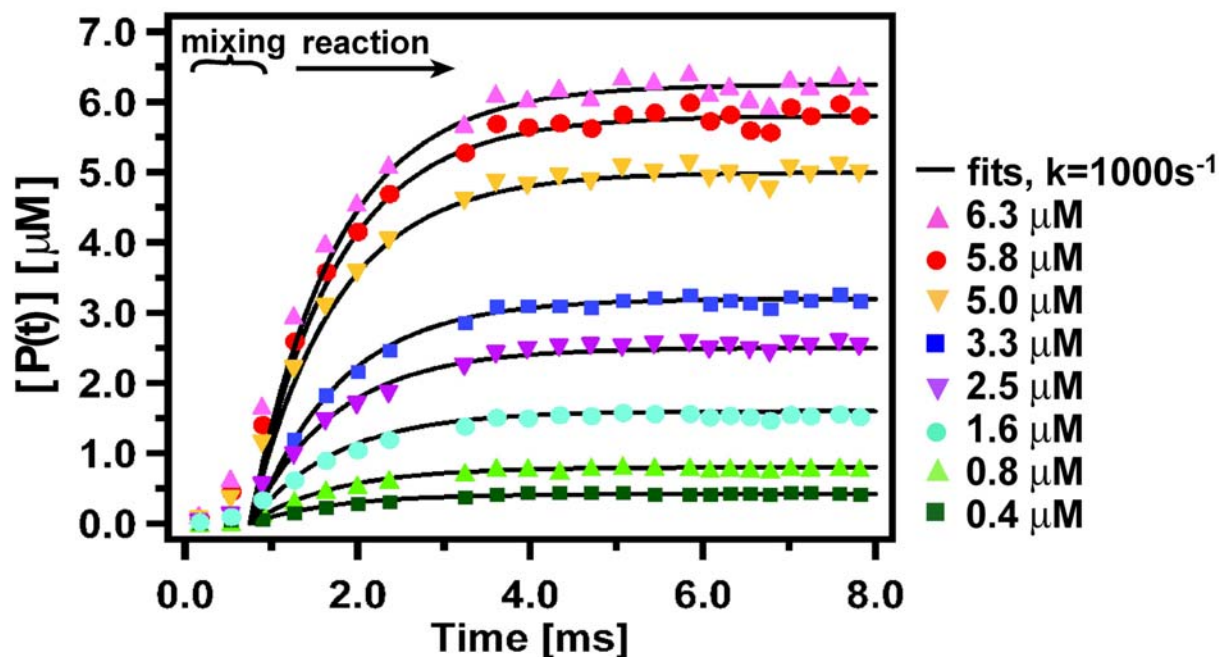


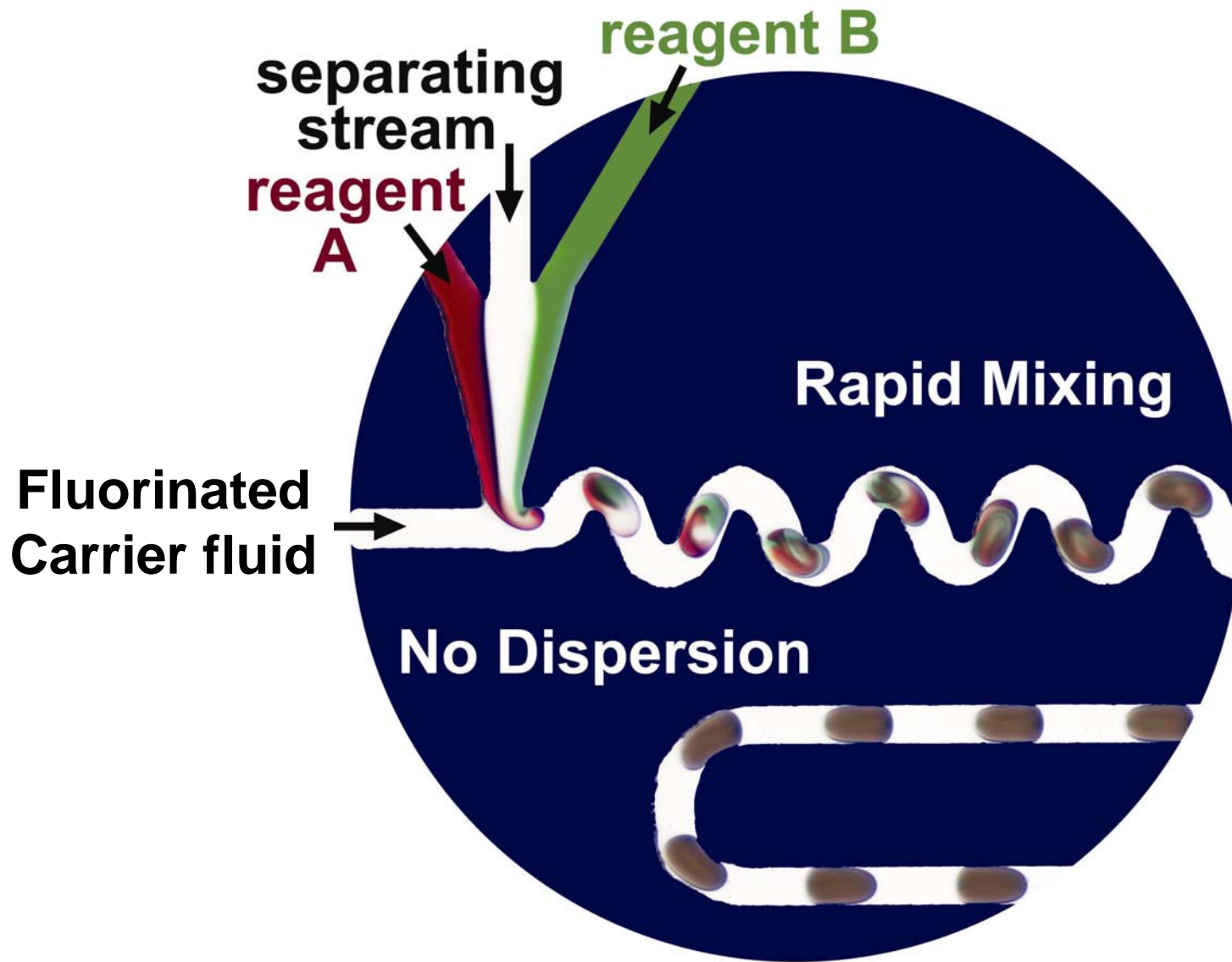
For single-turnover kinetics,
where $[E]_0 \gg [S]_0$:

$$[P(t)] = [S]_0 (1 - \text{Exp}(-k \times t))$$

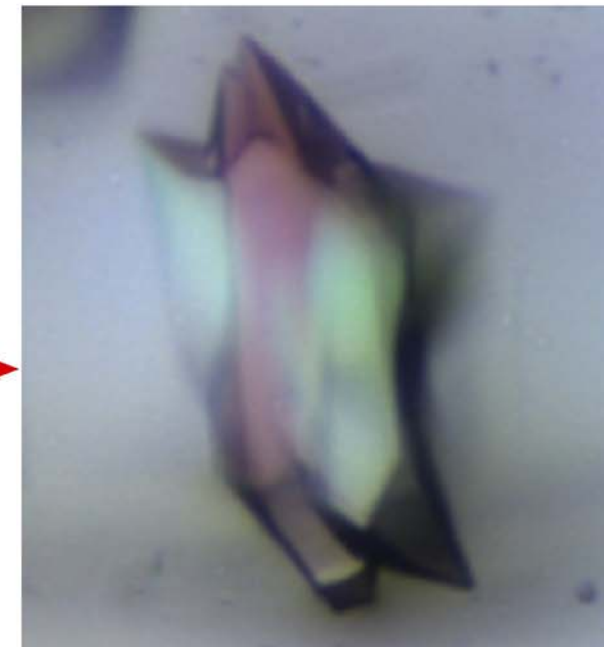
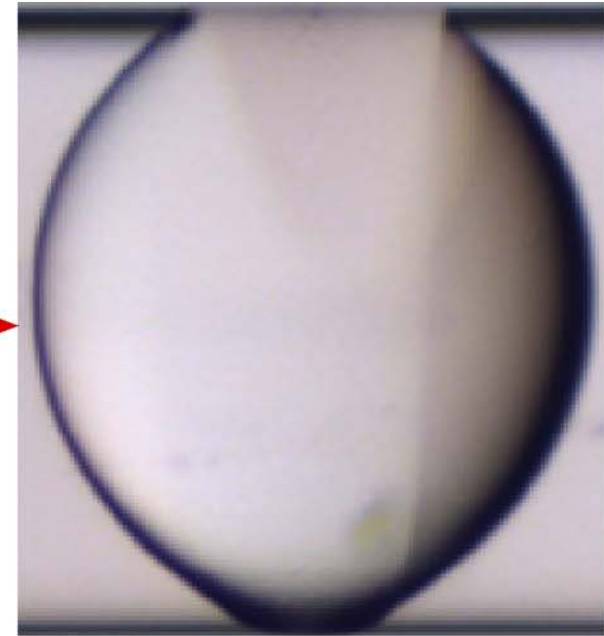
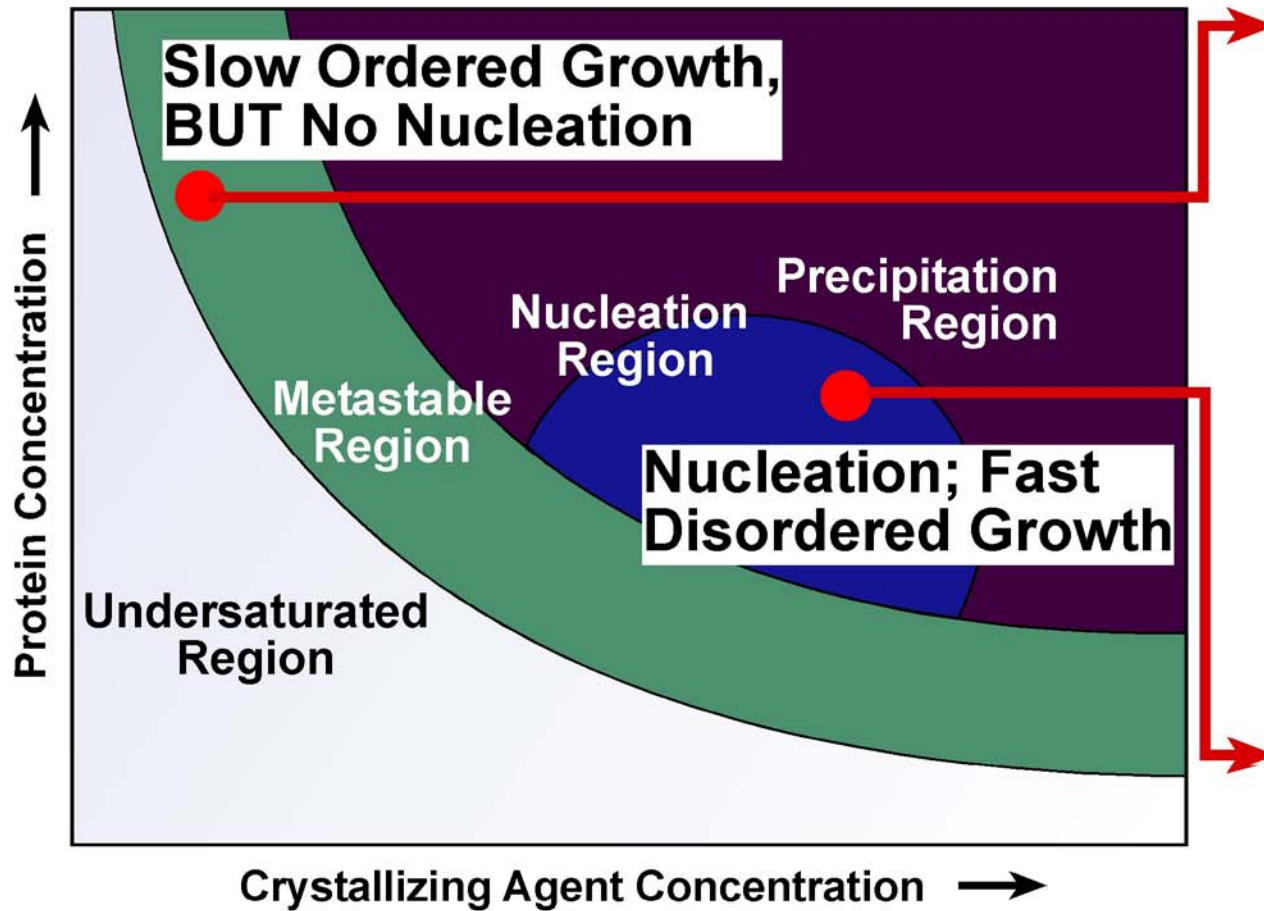
Sample consumption
33 nL/s

Used less than
1 μL total
of sample
for all
8 curves



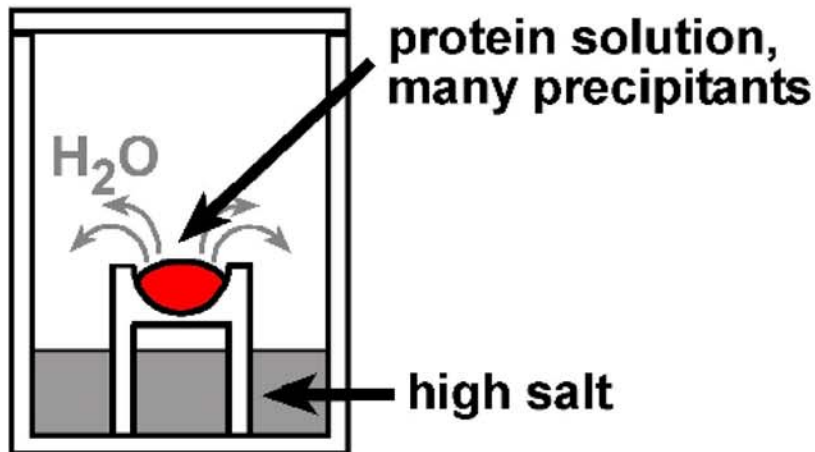


Protein crystallization is to recognize the right crystallizing agent and to the right concentration



Protein Crystallization is Commonly Done in 100 -1000 nL (1 μ L) **droplets**

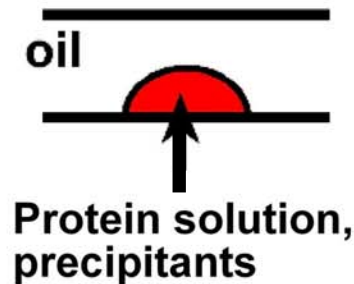
Vapor Diffusion



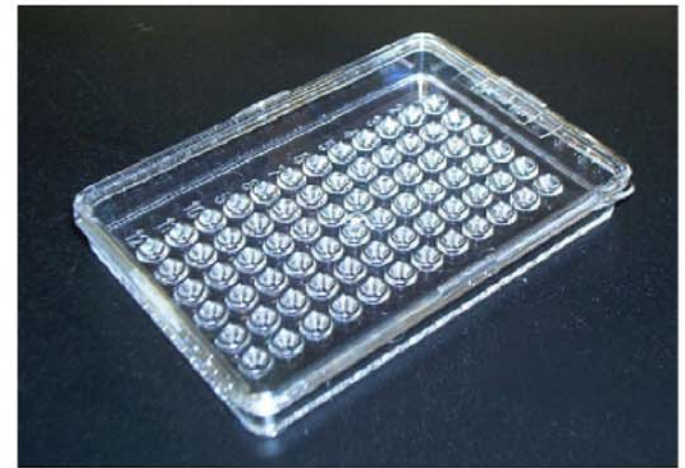
Optimal system:

- Many trials
- Low sample consumption
- Rapid
- **Broad and dense coverage of space**
- **No evaporation**
- **Reproducibly generates trials**
- **Reliably handles membrane protein**

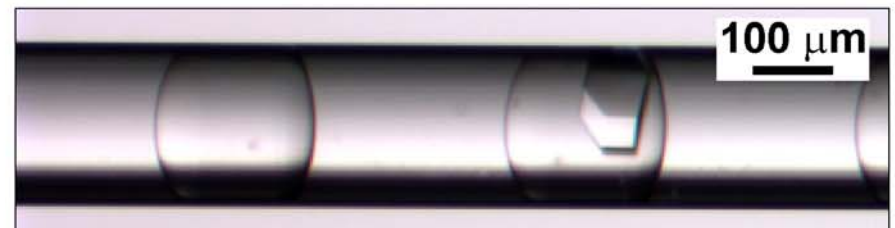
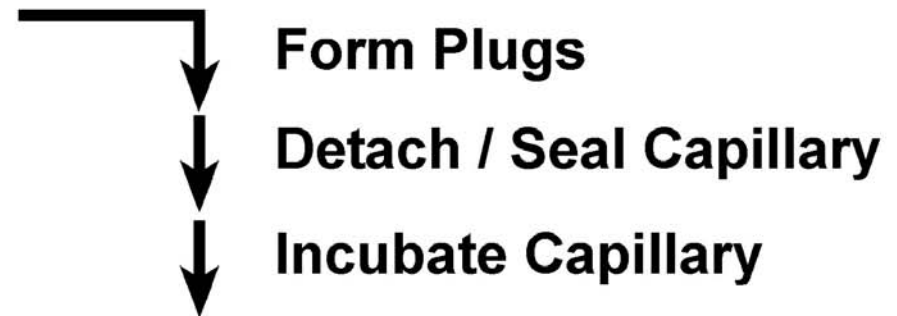
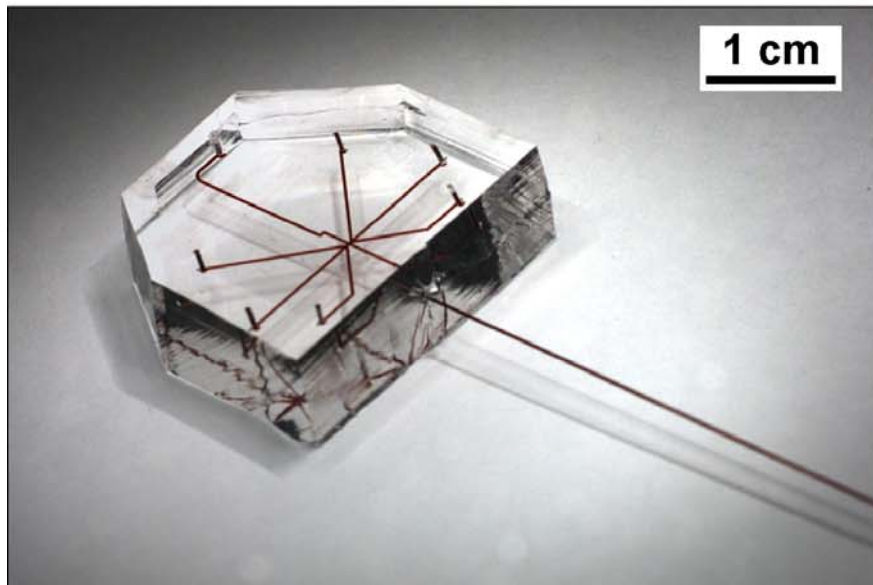
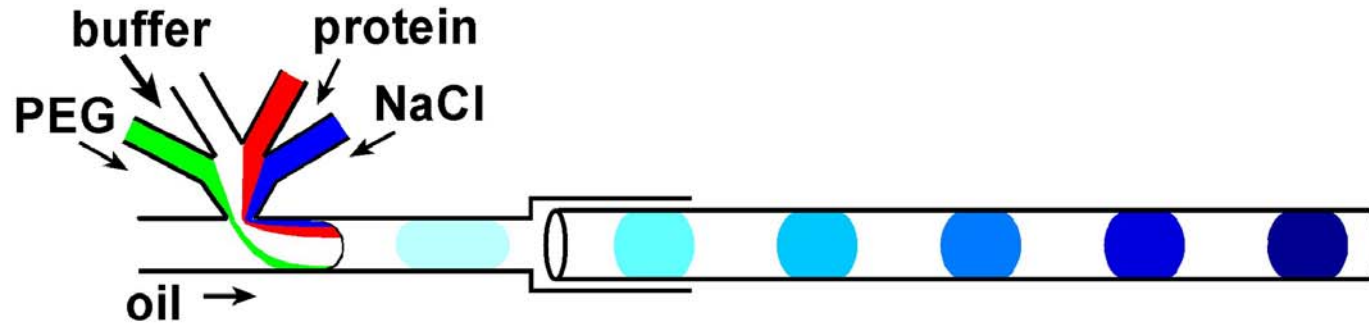
Microbatch



Microbatch Plate

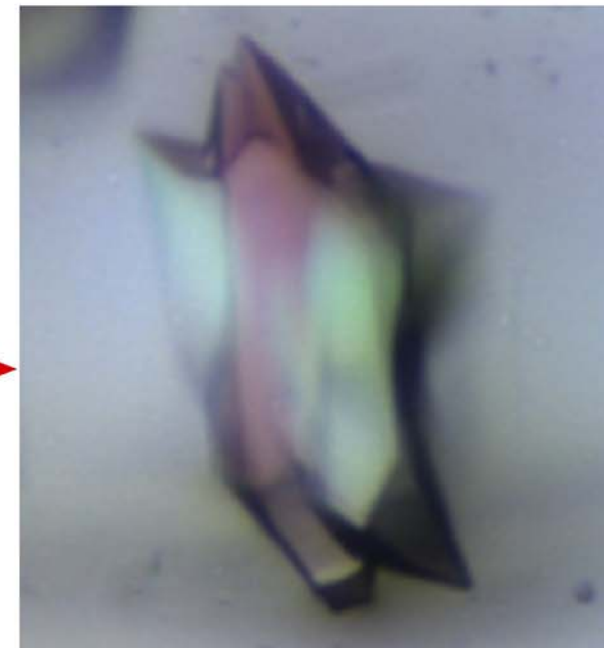
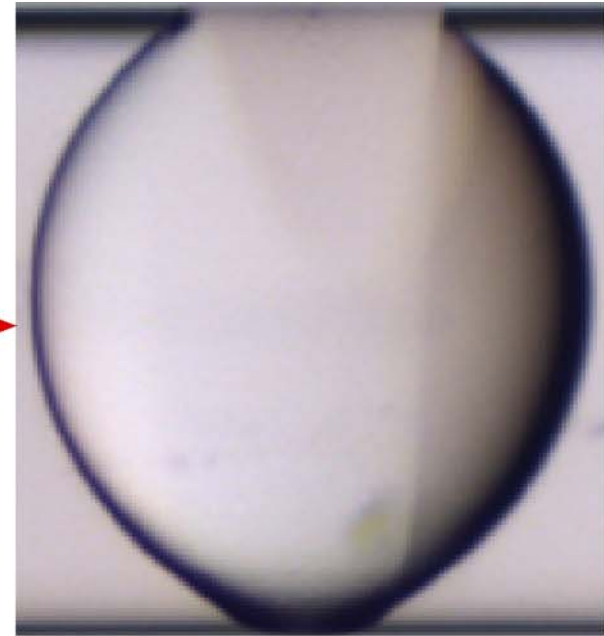
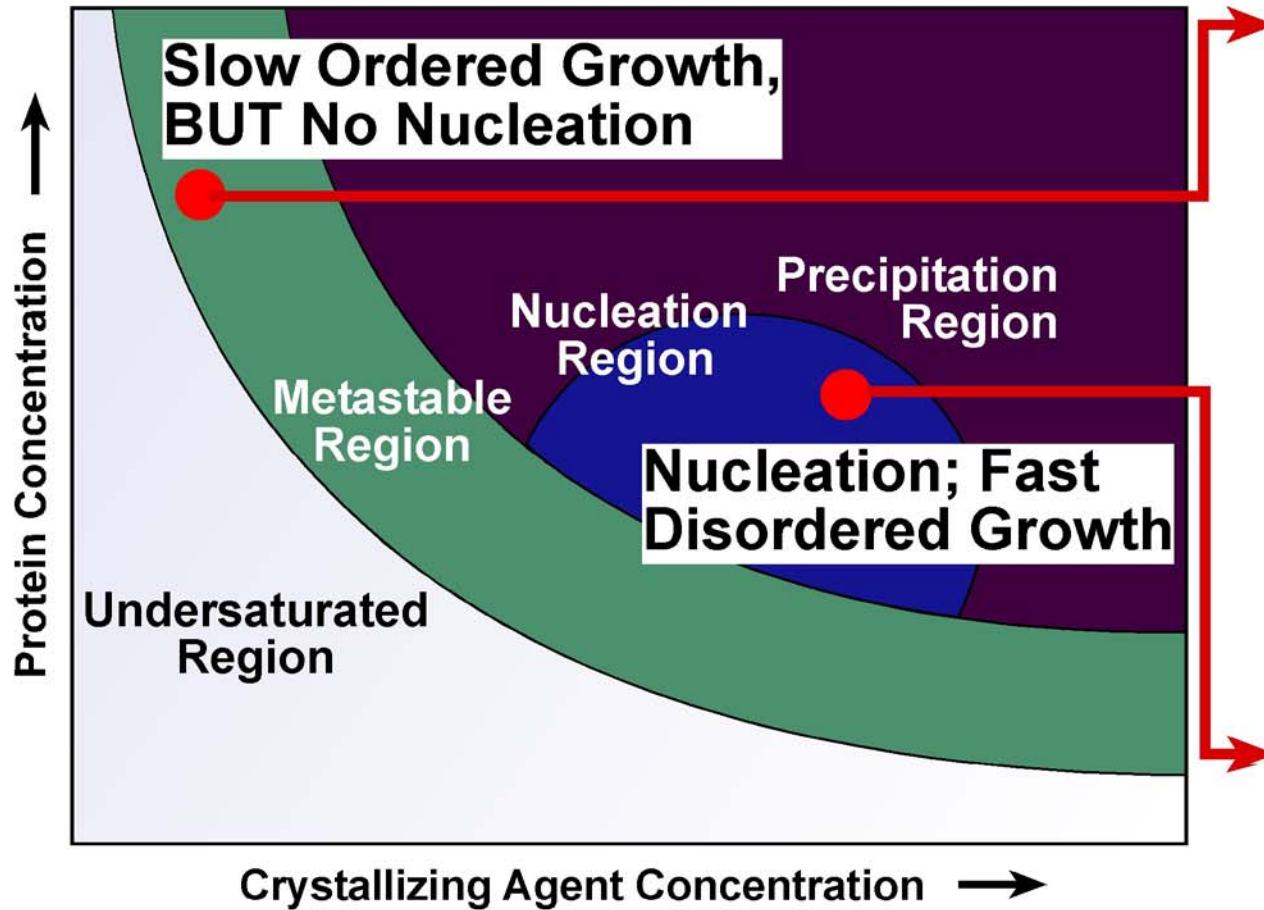


Crystallization in X-ray Capillaries: No Evaporation

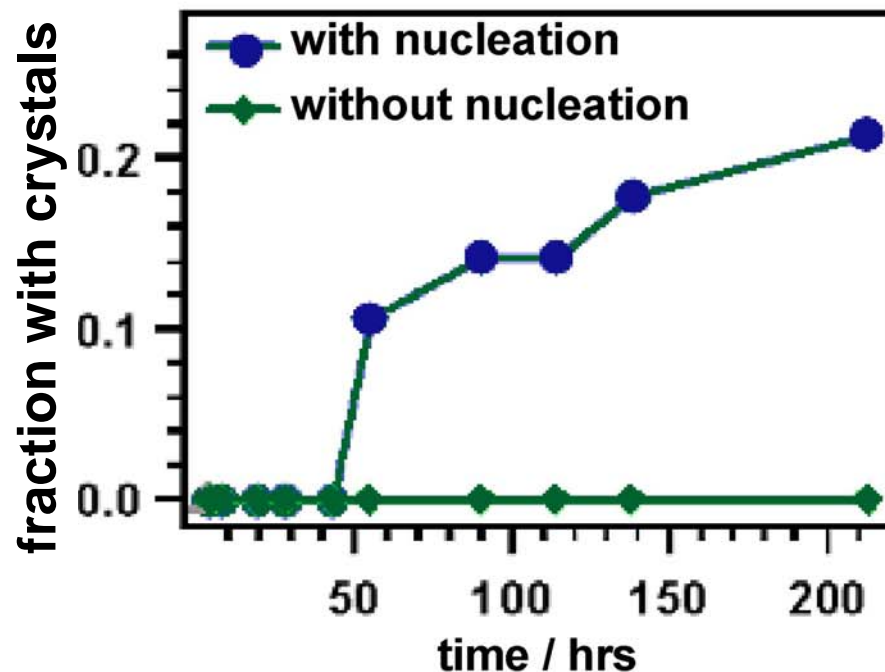
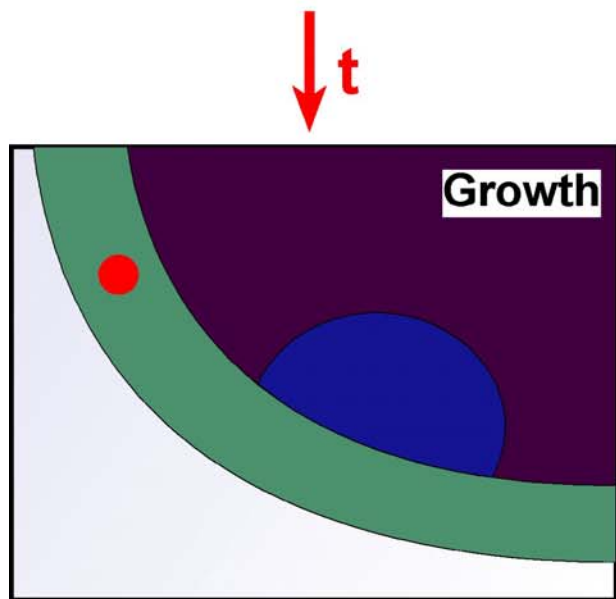
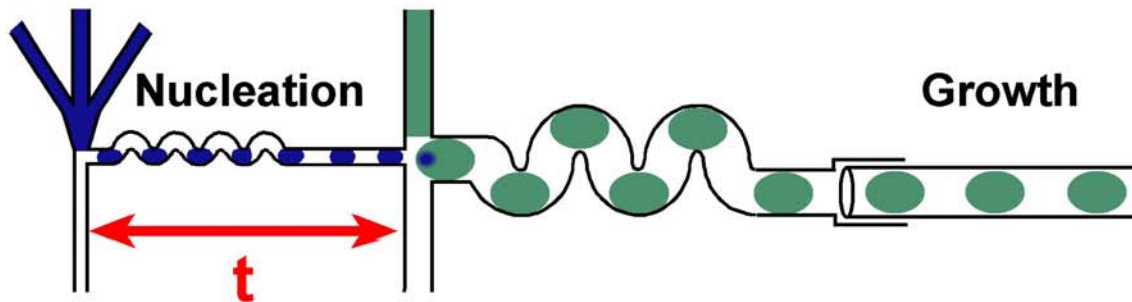
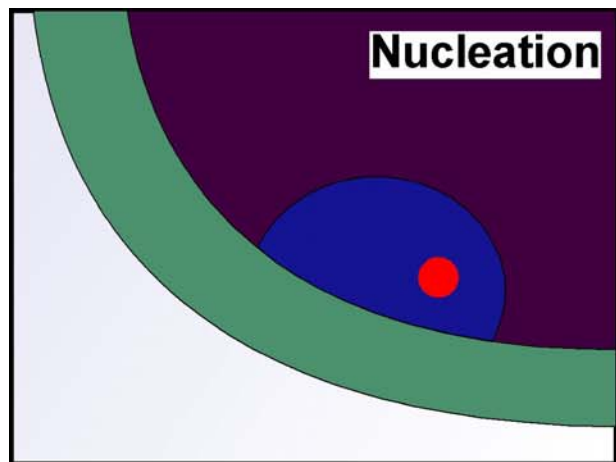


Stable for over a year

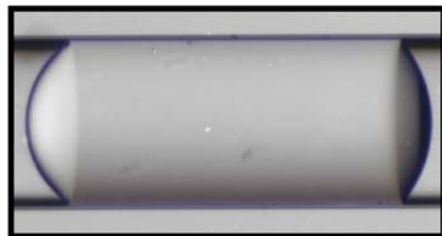
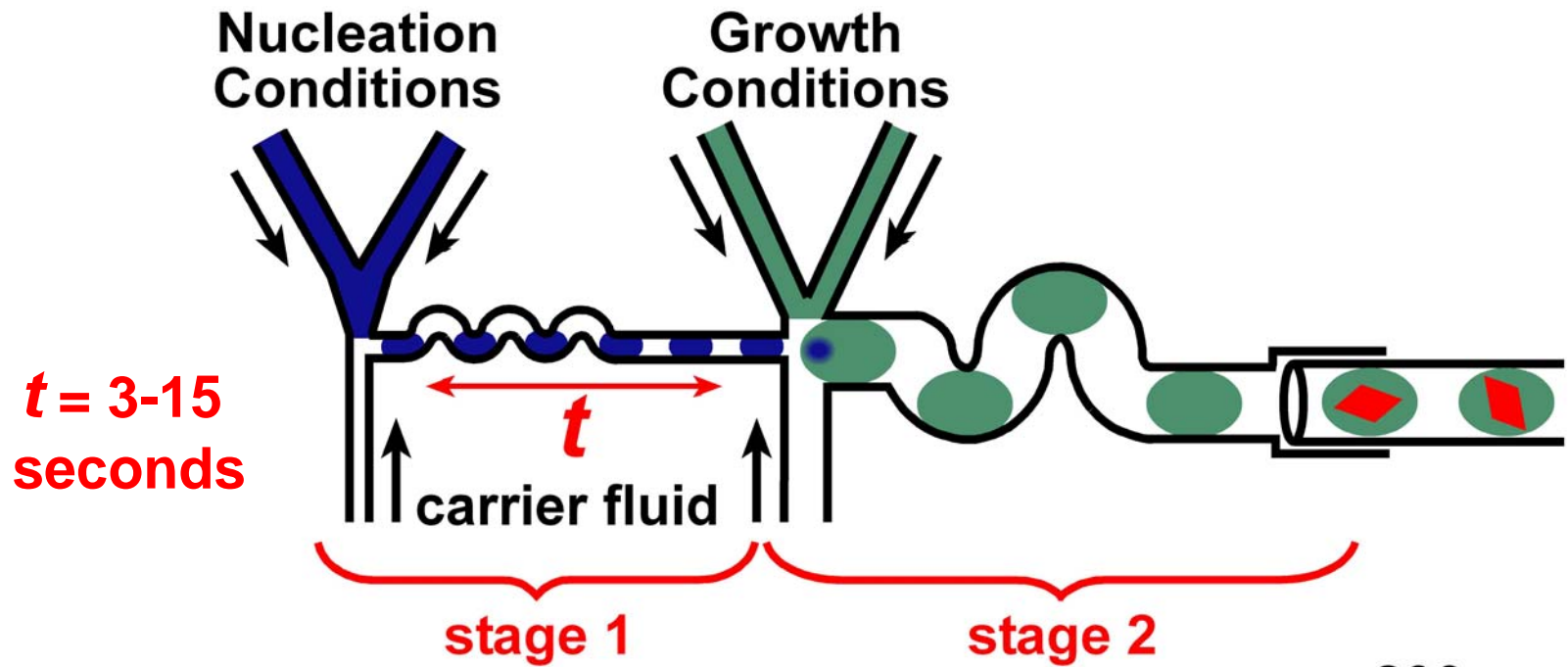
*In crystallization
You get nucleation
Or ordered growth --
But rarely both*



Independent Control of Nucleation and Growth Using Time and Concentration Control



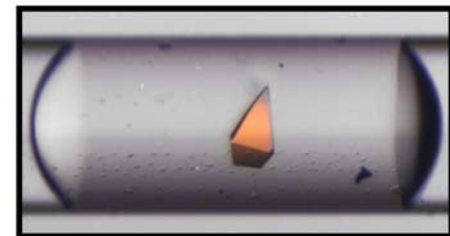
Separation of Nucleation and Growth - Microfluidic Seeding



growth
conditions only



nucleation
conditions only



nucleation and
growth combined

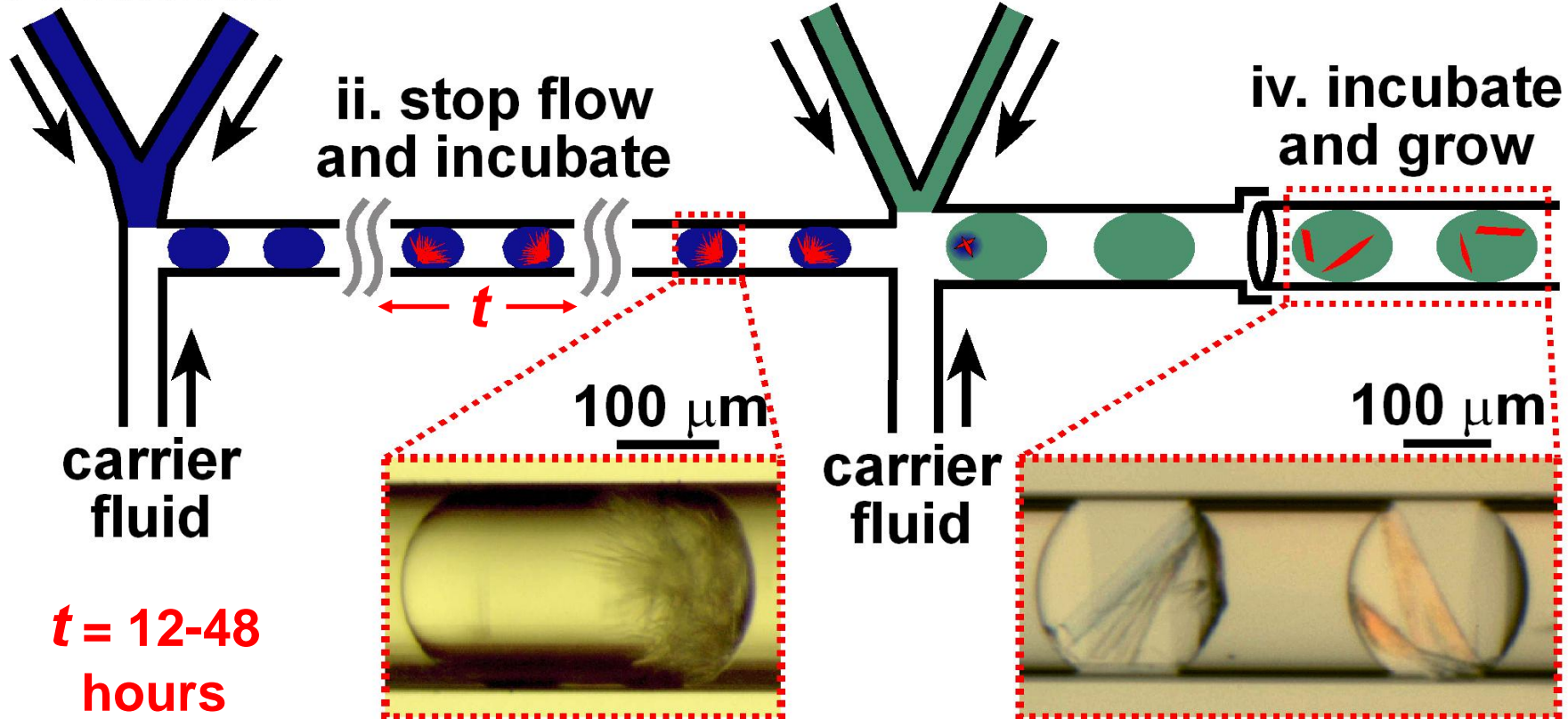
Microfluidic Seeding with SARS Nucleocapsid N-terminal Domain

i. start with nucleation conditions

iii. seed the growth conditions

ii. stop flow and incubate

iv. incubate and grow



Crystallization of Oligoendopeptidase F - Microfluidic Seeding

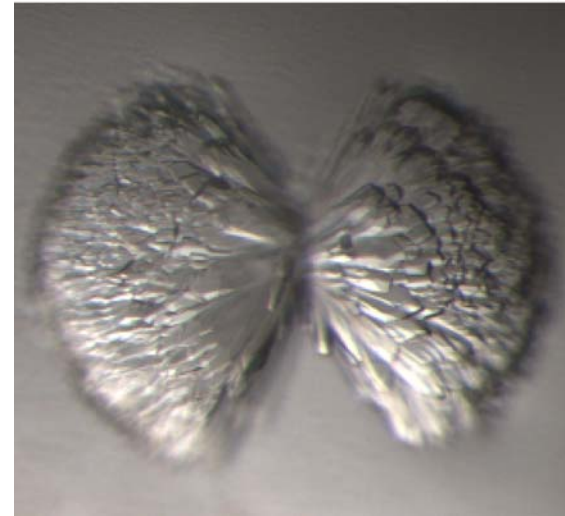
Precipitation in VD drop

100 μm



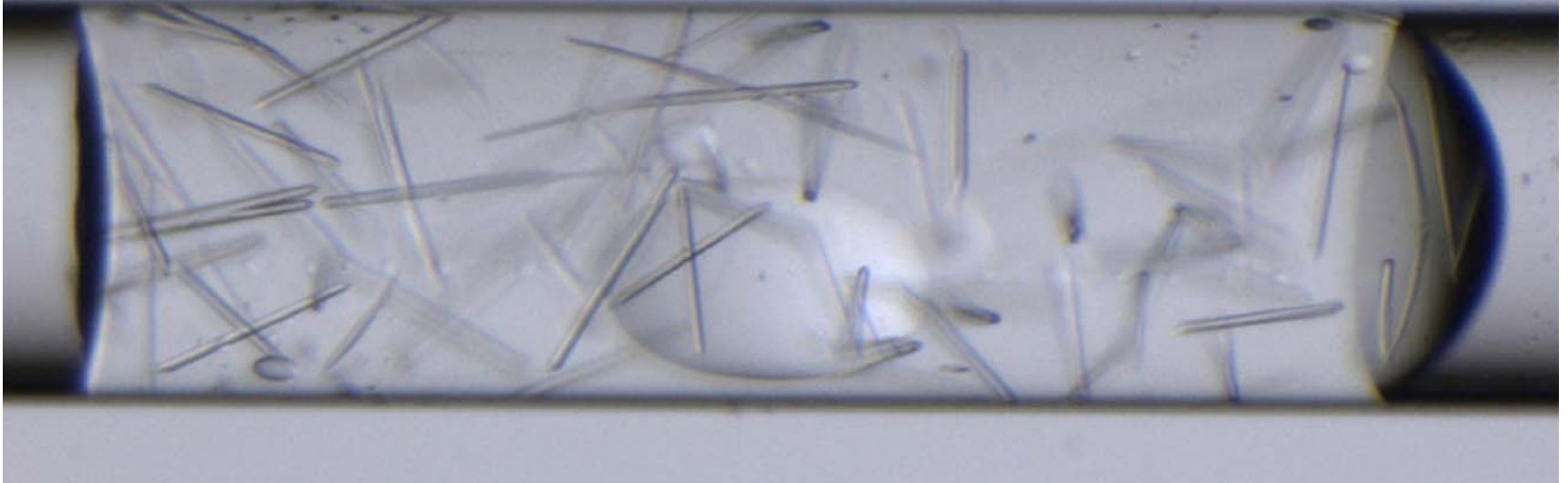
Clusters in VD drop

100 μm



100 μm

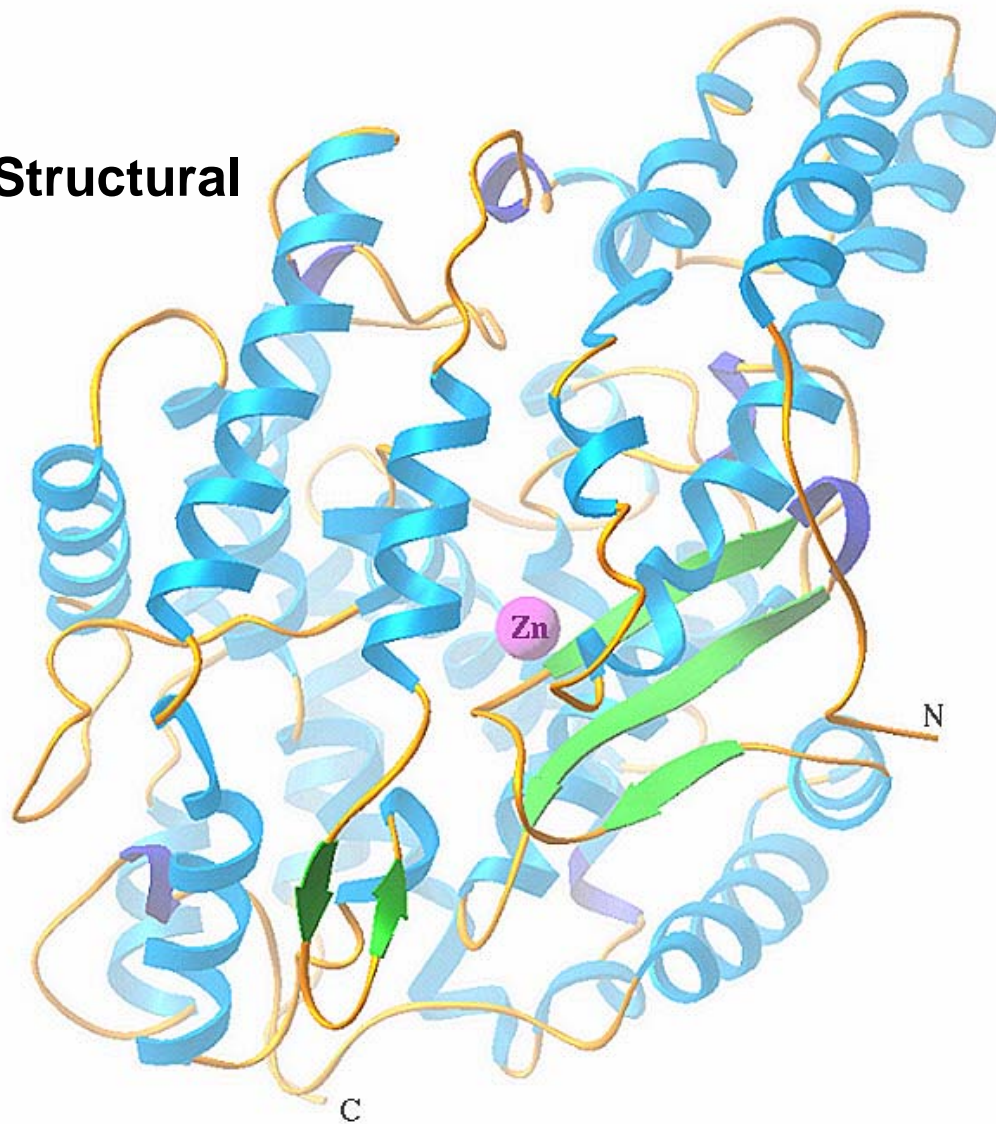
Single crystals using microfluidic seeding



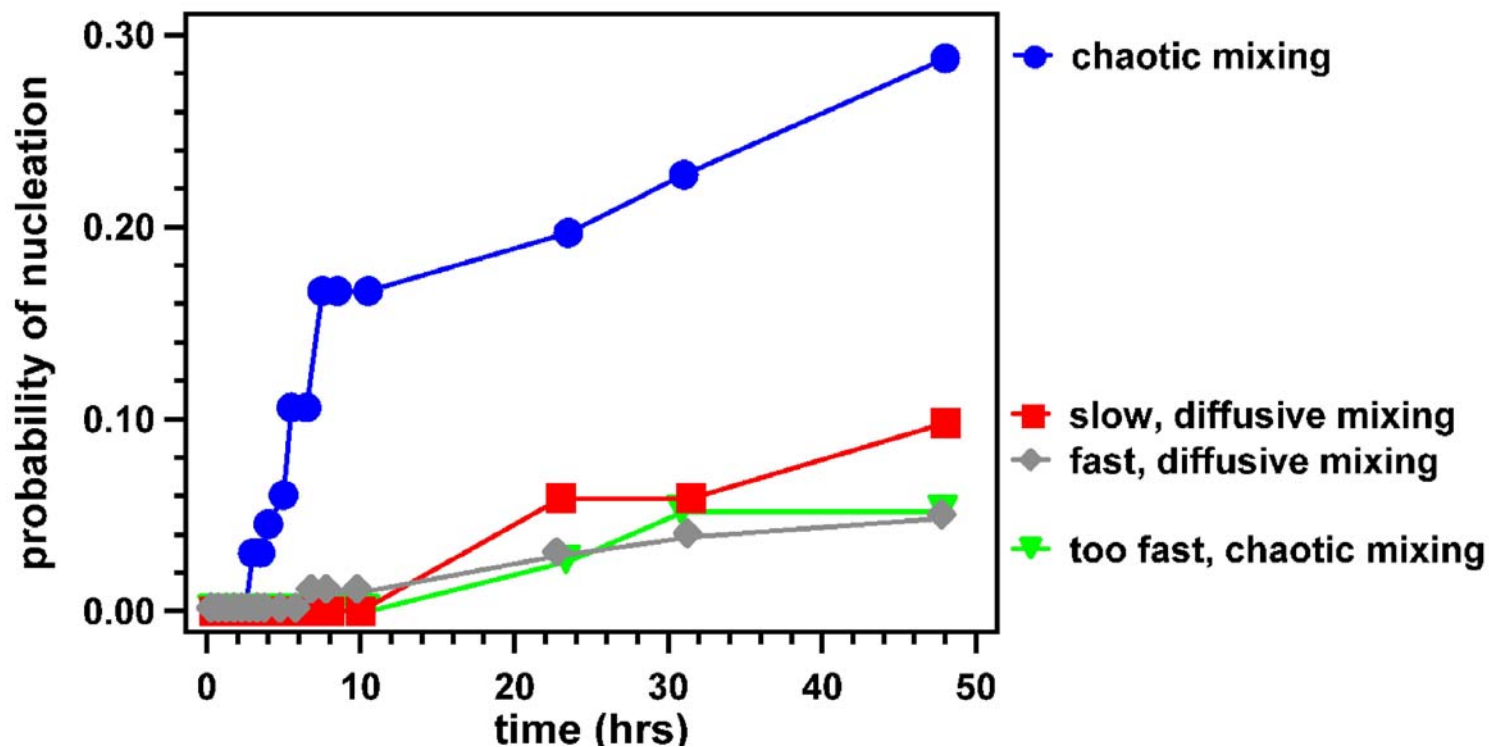
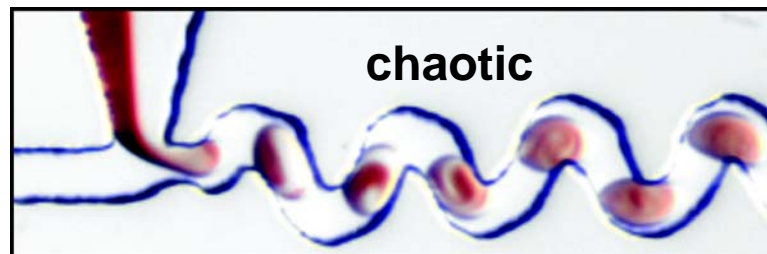
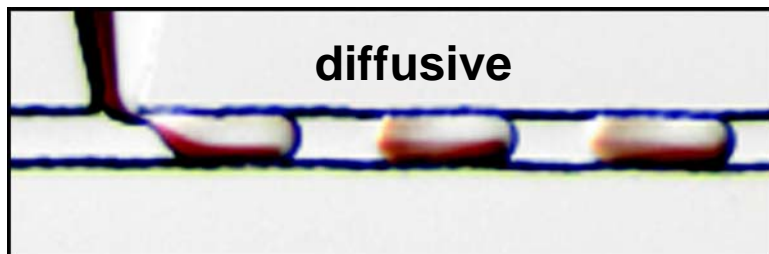
Data Collection - Structure Determination

- metallopeptidase family M3
- selected by Midwest Center for Structural Genomics but unsolved and set aside

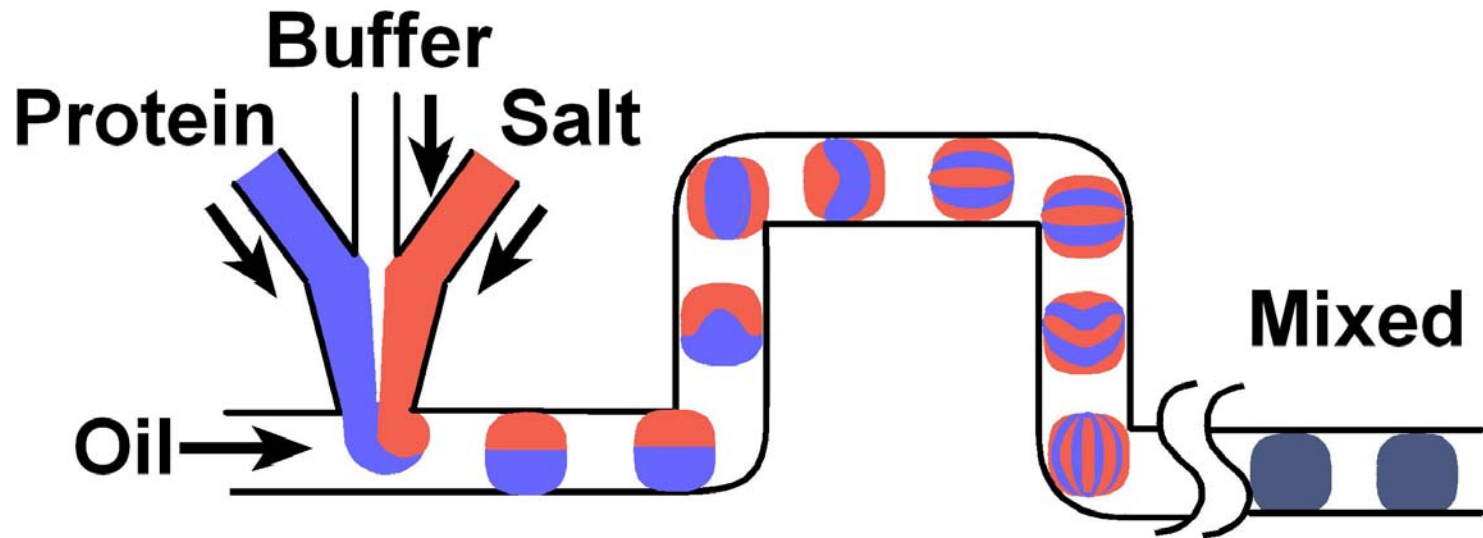
- solved by SAD technique
- 3.1 Å resolution
- Space group: P3121; Unit Cell
- Parameters $a=b$ 119.50 $c=248.90$
- R-factor = 0.196, R_{free} = 0.248
- Solvent Content: ~70%;



Mixing is also Important for Protein Crystallization: Effective Nucleation by Slow Chaotic Mixing



Understanding the Mixing Effect with a Chaotic Mixing Model



Assumption:
Only nucleation at
interfaces is important

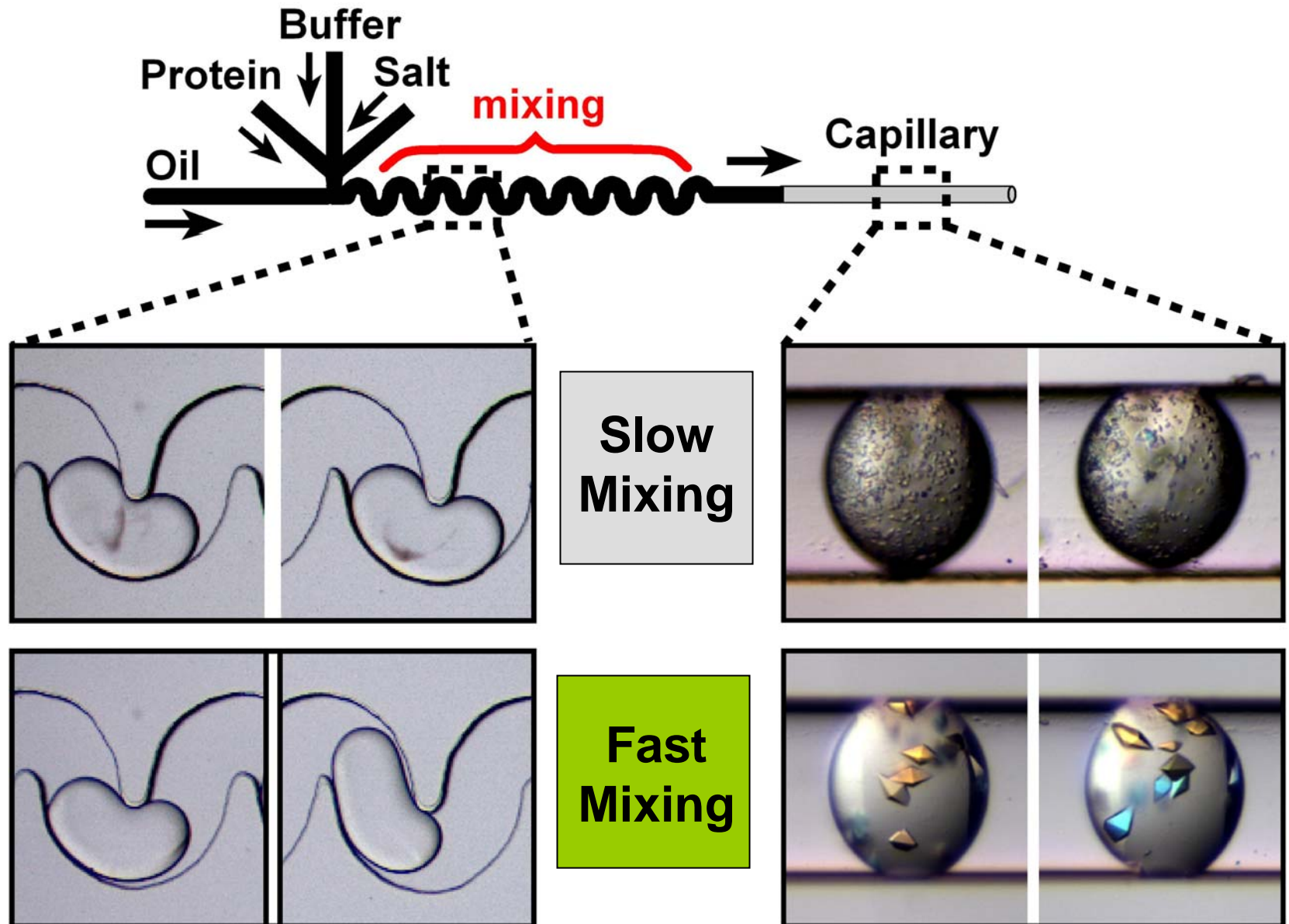
**Slow
Mixing**

**Lifetimes
of Interfaces
are long**

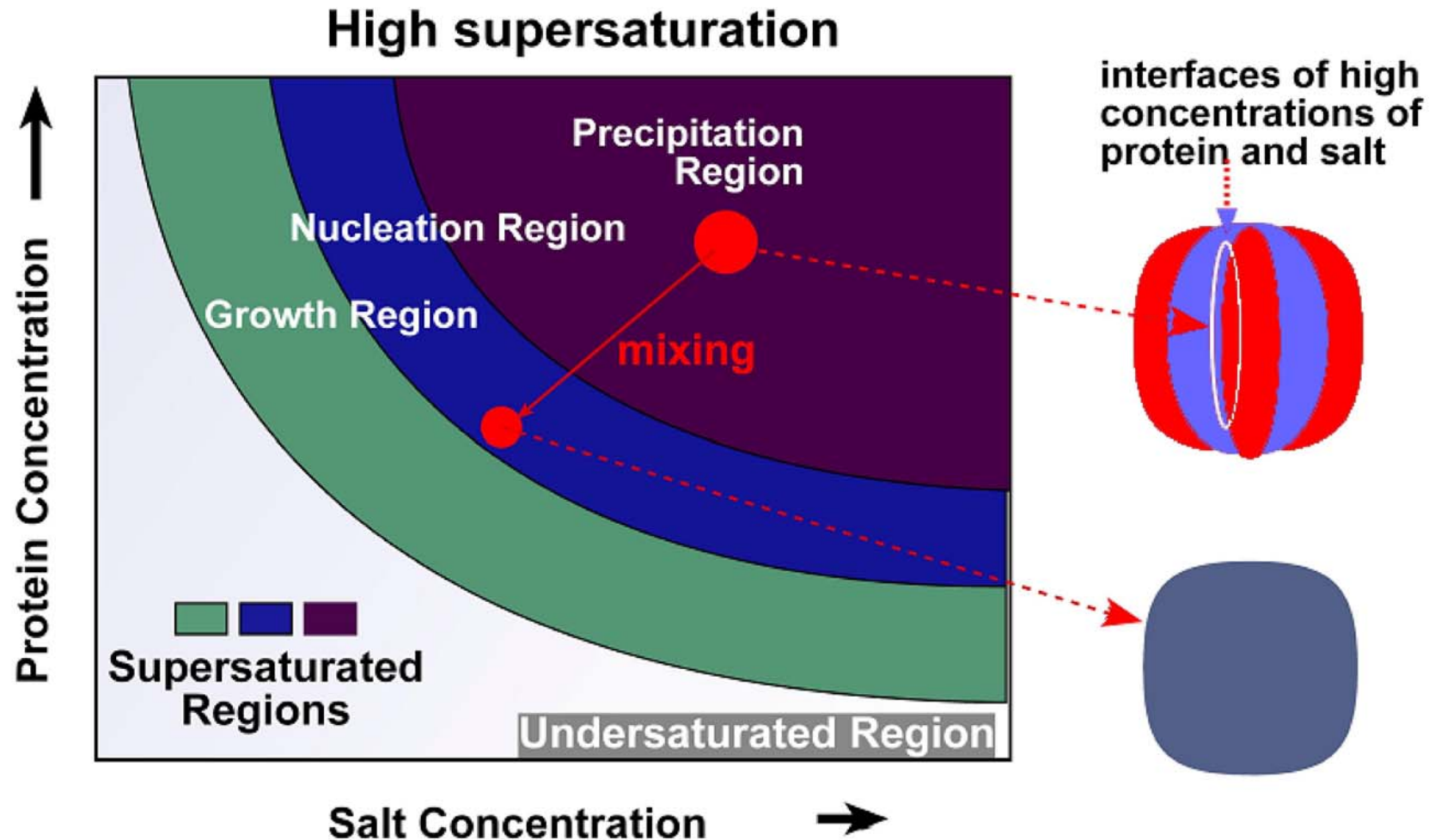
**Fast
Mixing**

**Lifetimes
of Interfaces
are short**

Experimental Results: Mixing Effect at High Supersaturation



Protein Crystallization Phase Diagram: Time Dependent



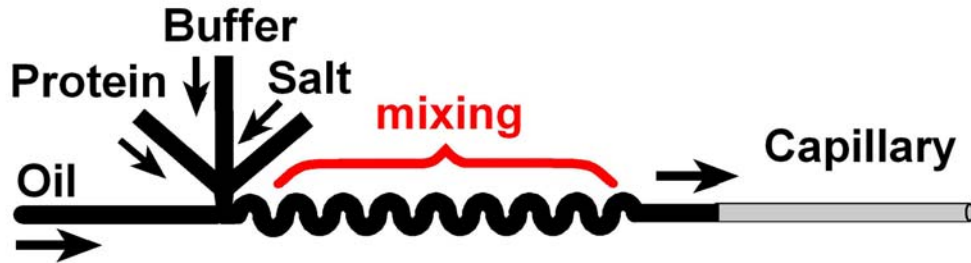
Slow Mixing:

Precipitation happens faster than mixing

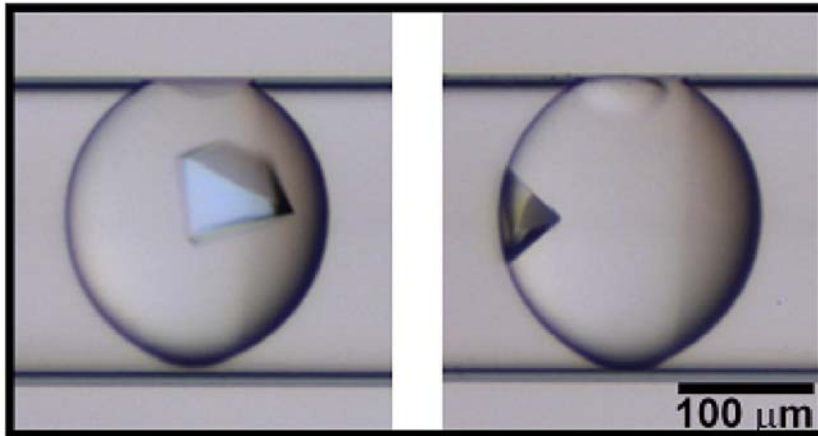
Fast Mixing:

Mixing happens faster than precipitation

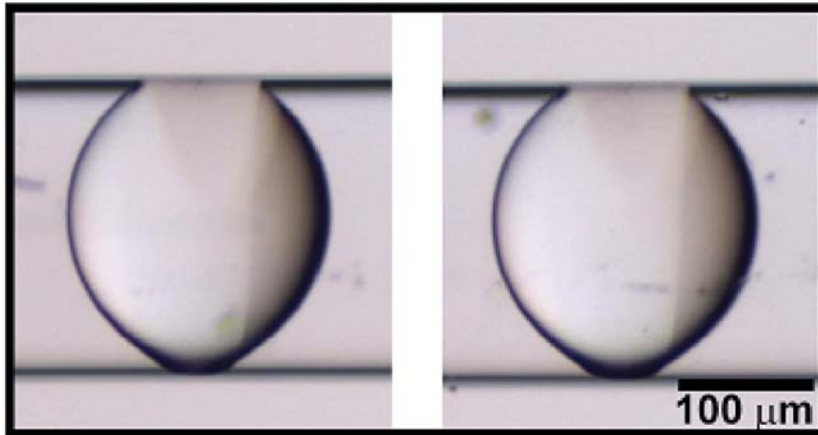
Experimental Results: Mixing Effect at Low Supersaturation



No crystals may mean improper mixing instead of a bad precipitant

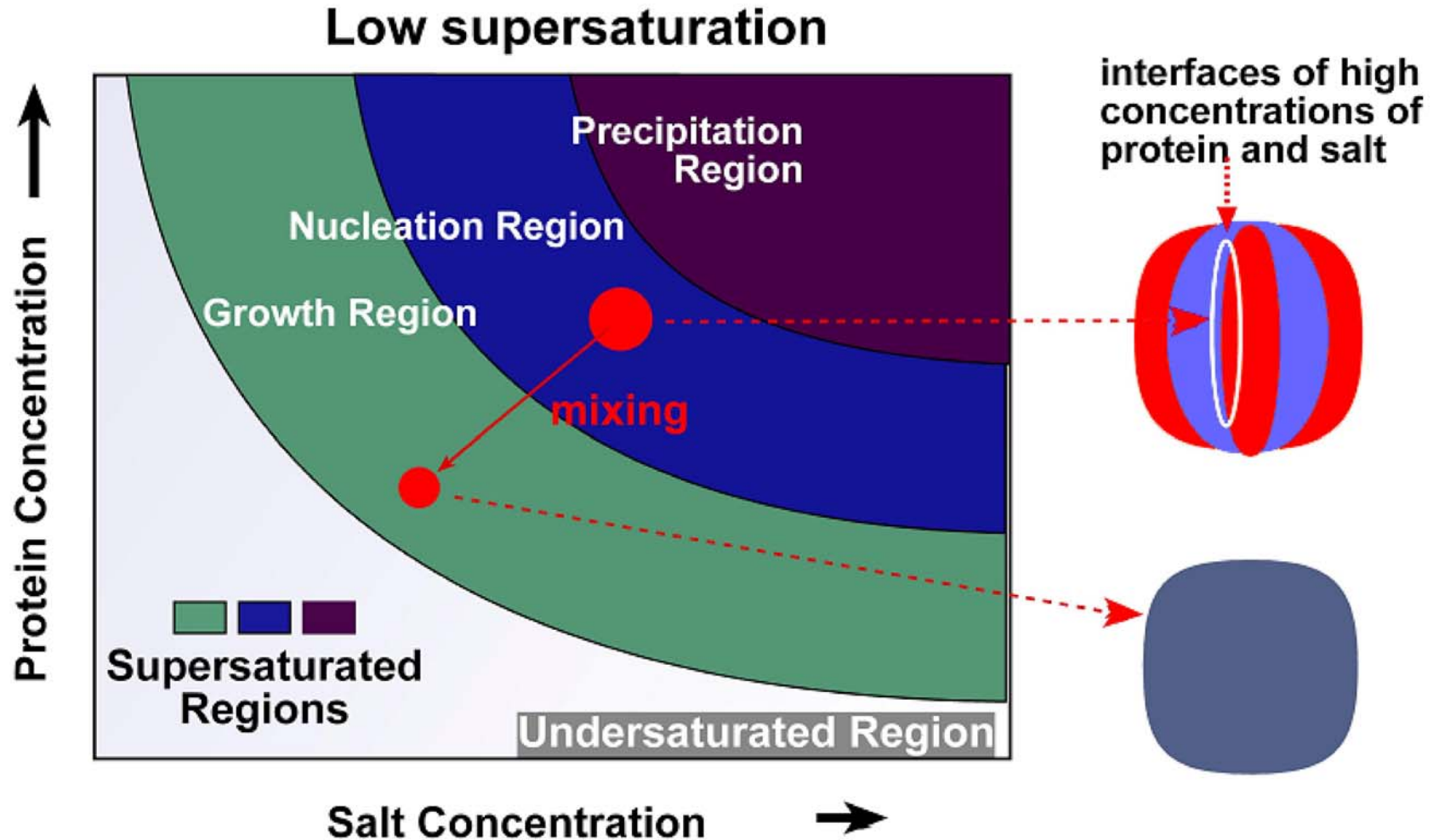


Slow
Mixing



Fast
Mixing

Protein Crystallization Phase Diagram: Time Dependent



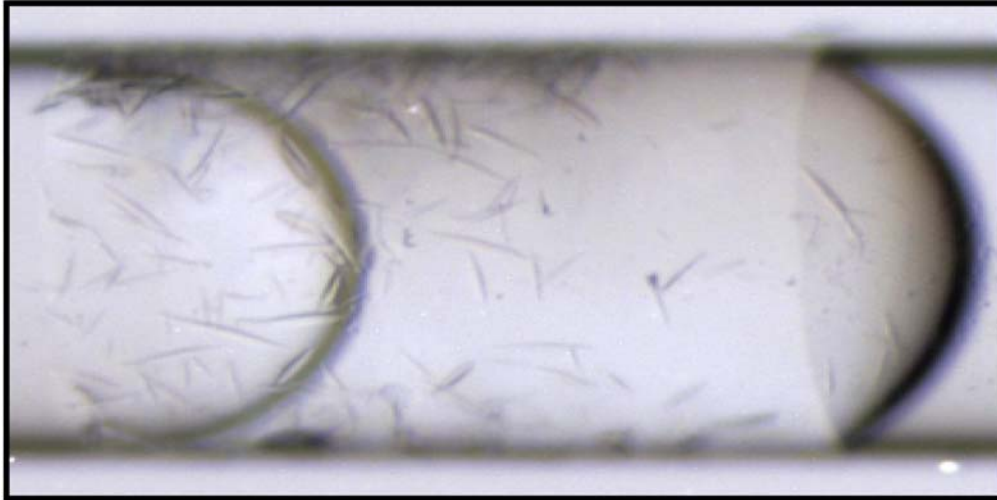
Slow Mixing:

Nucleation happens faster than mixing

Fast Mixing:

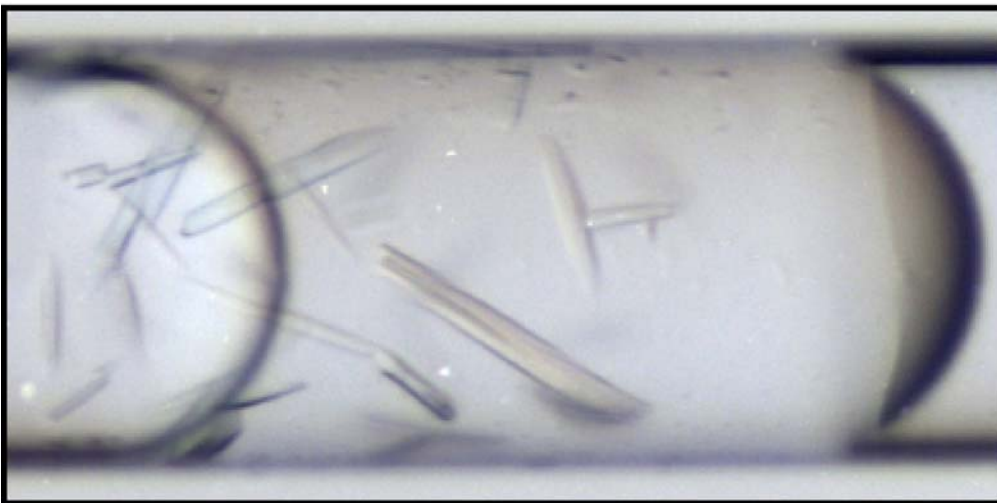
Mixing happens faster than nucleation

Mixing Effect in the Crystallization of a Novel Protein



**Slow
Mixing**

many crystals

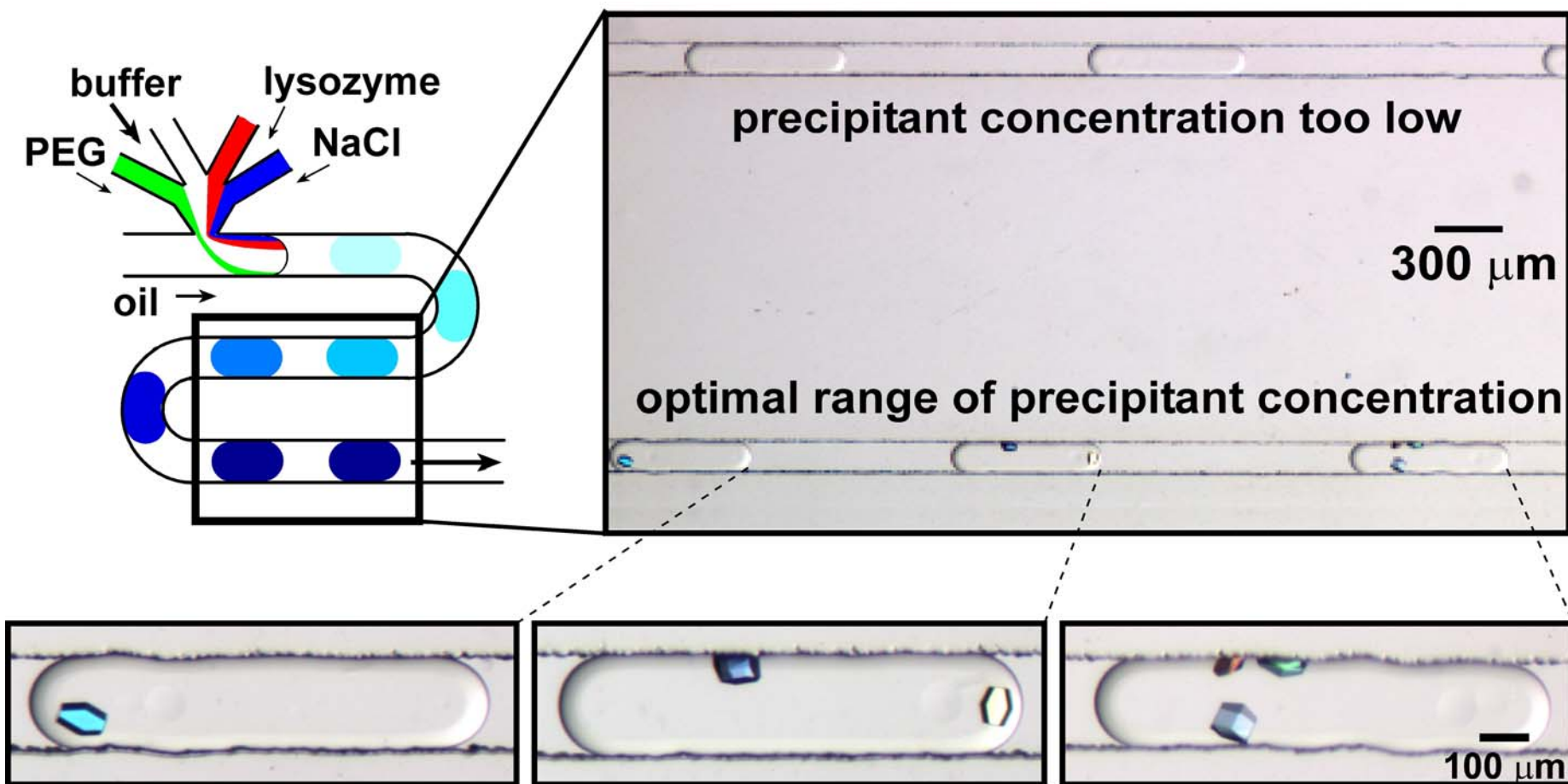


**Fast
Mixing**

few crystals

Developing Microfluidic Tools to Screen Protein Crystallization Conditions

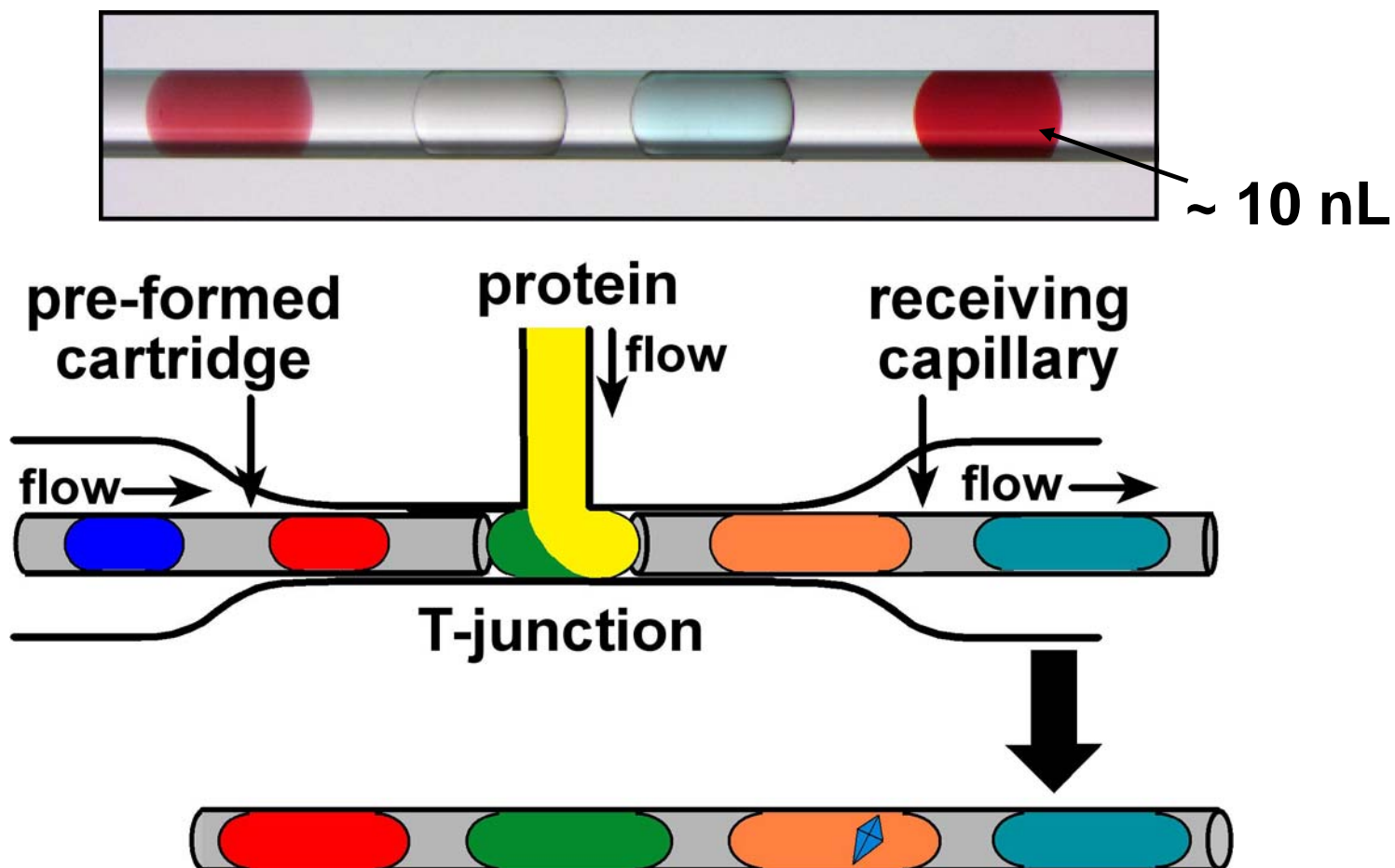
1. Gradient Screen of Crystallization Conditions



Developing Microfluidic Tools to Screen Protein Crystallization Conditions

2. Sparse Matrix Screen in Nanoliter Plugs

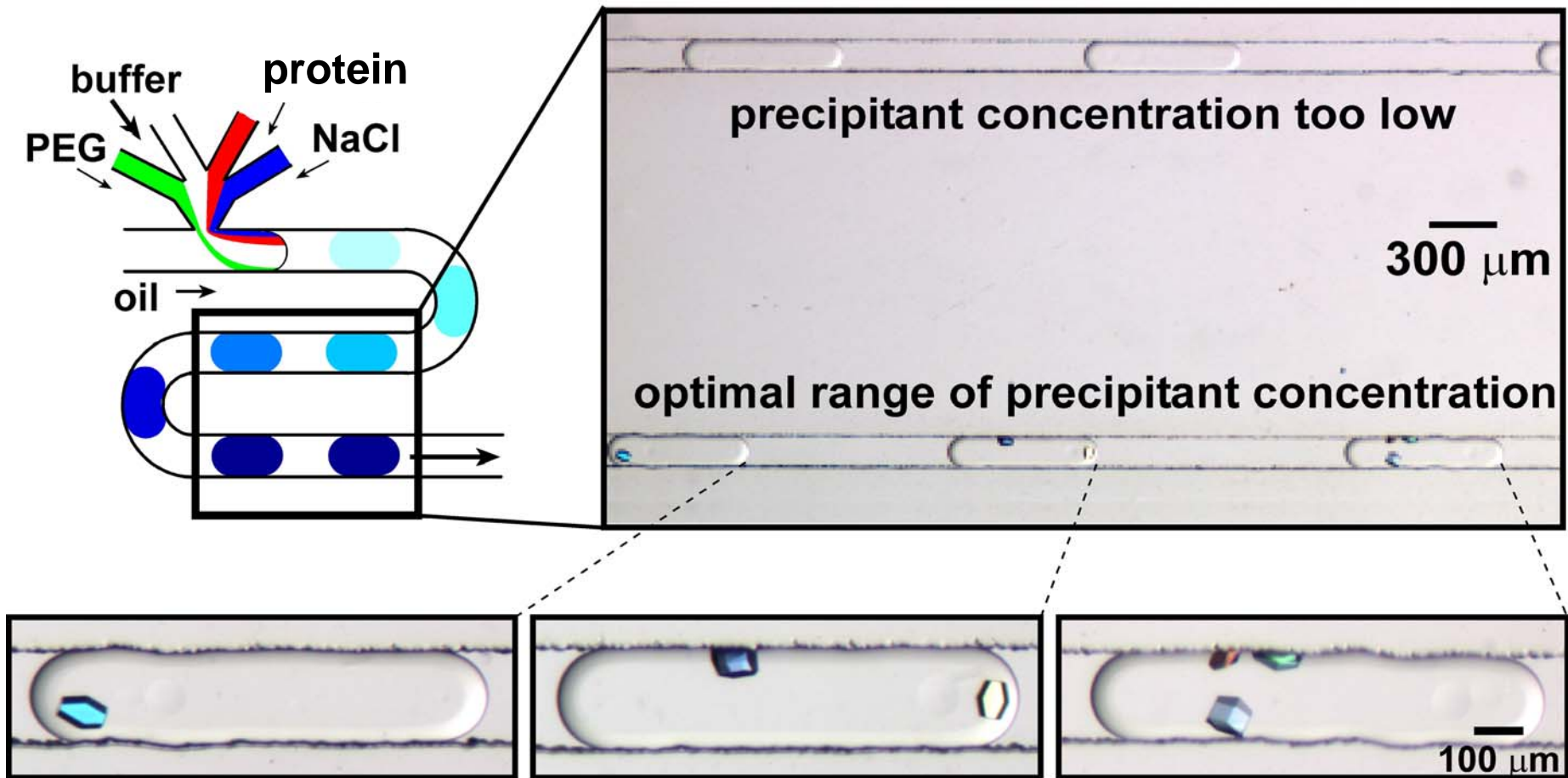
Pre-formed Cartridge



Crystallization of Membrane Proteins

- ❖ **Determining crystal structure of membrane protein: focus of major research efforts.**
 - Important signaling functions
 - Targets of >50% drugs
- ❖ **Crystallization of membrane protein: big challenge**
 - Low in quantity, unstable over time.
 - Search of crystallization conditions: **Broad and dense**
- ❖ **Two Challenges on **handling membrane proteins****
 - High viscosity
 - Low surface tension

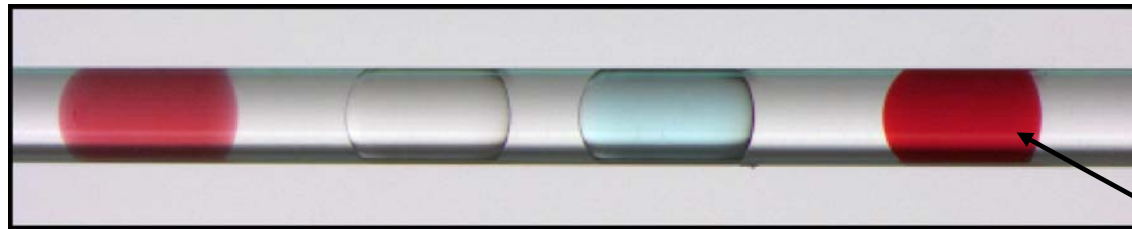
Gradient Screen of Crystallization Conditions



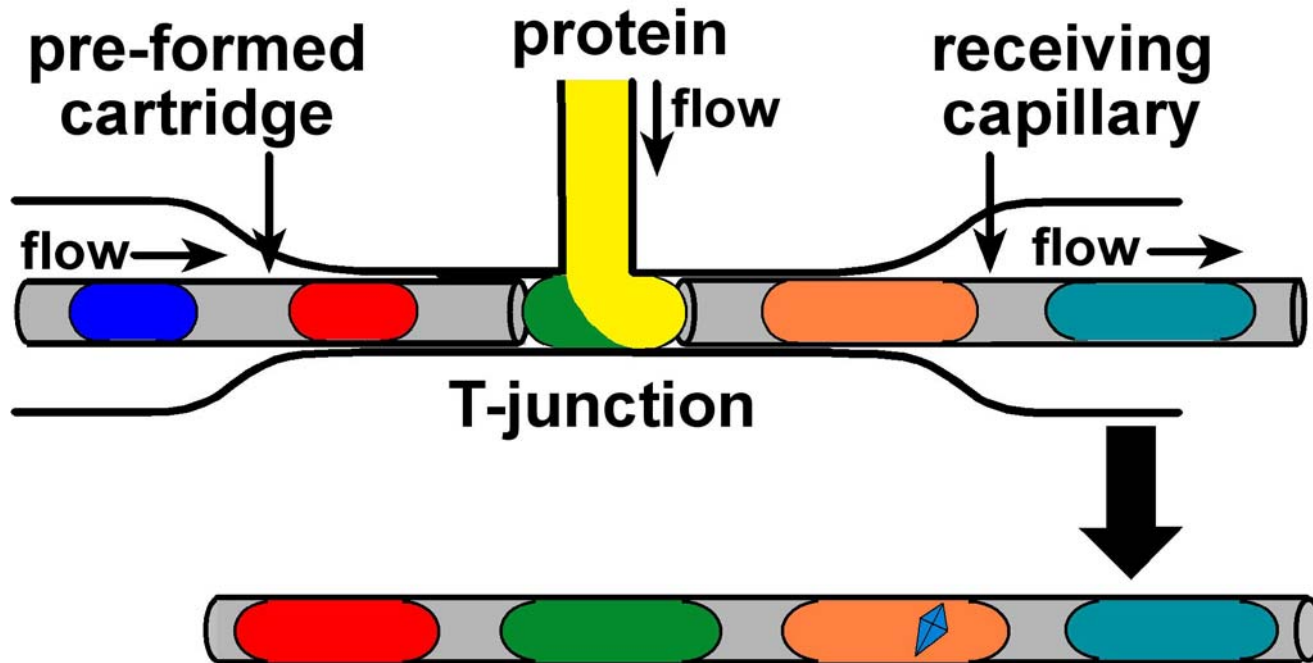
Dense but NOT Broad !

Sparse Matrix Screening in Nanoliter Plugs

Pre-formed Cartridge

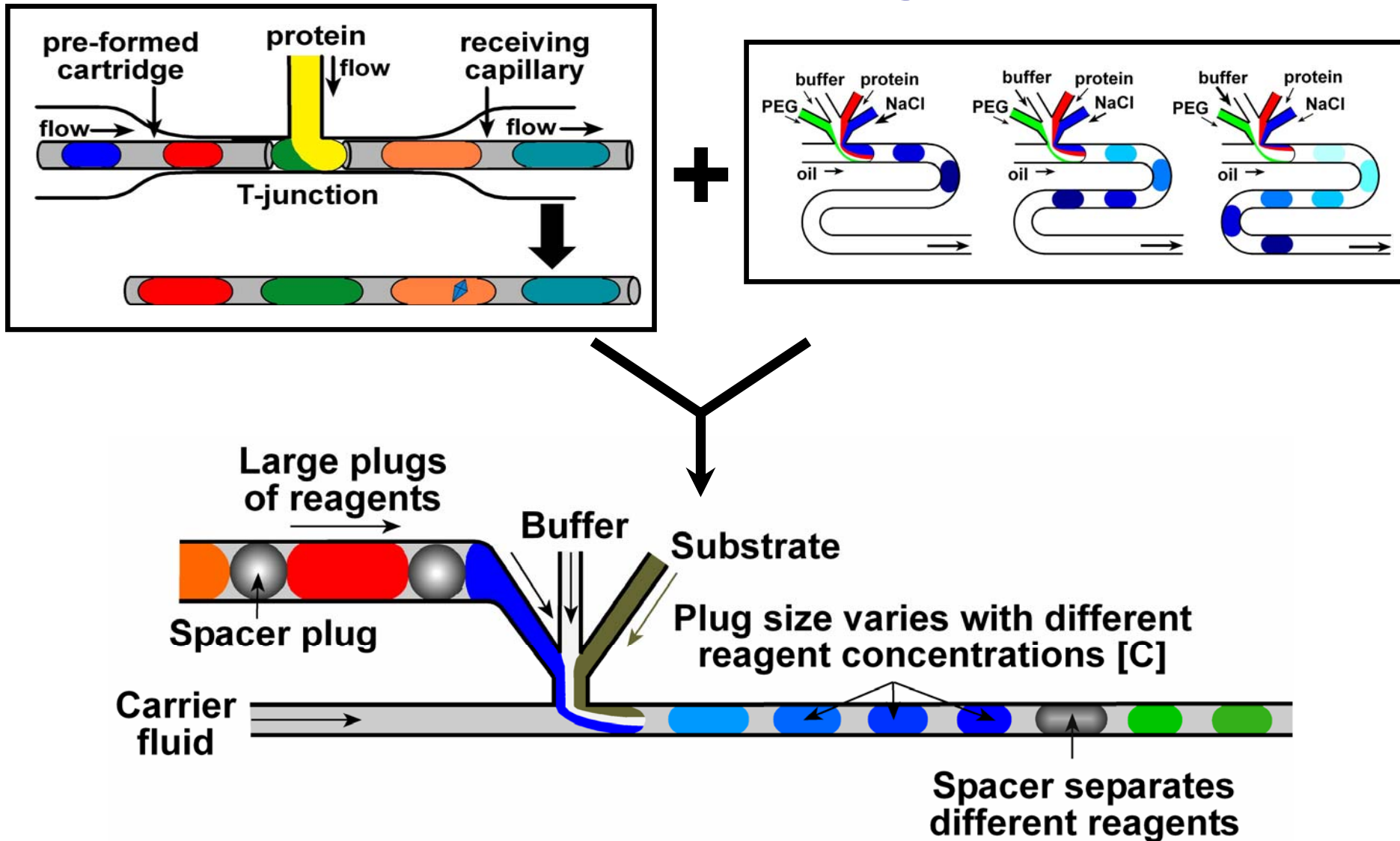


~ 10 nL



Broad but NOT Dense !

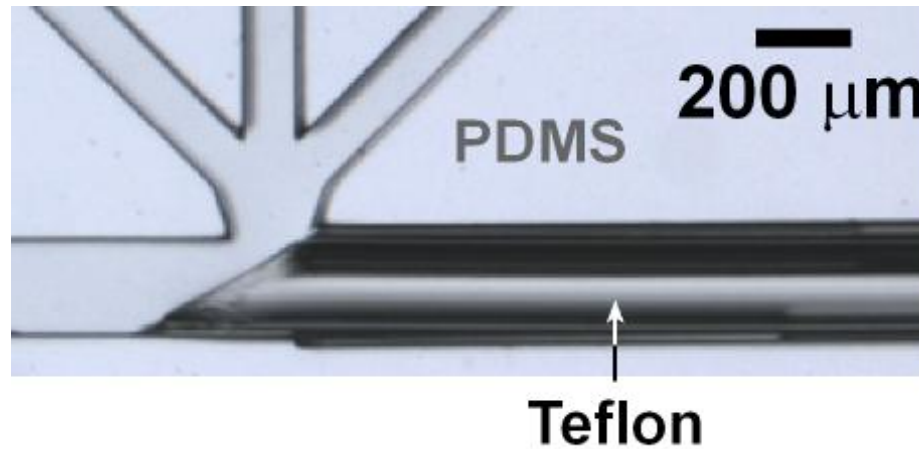
Hybrid Method: Combining Sparse Matrix and Gradient Screening



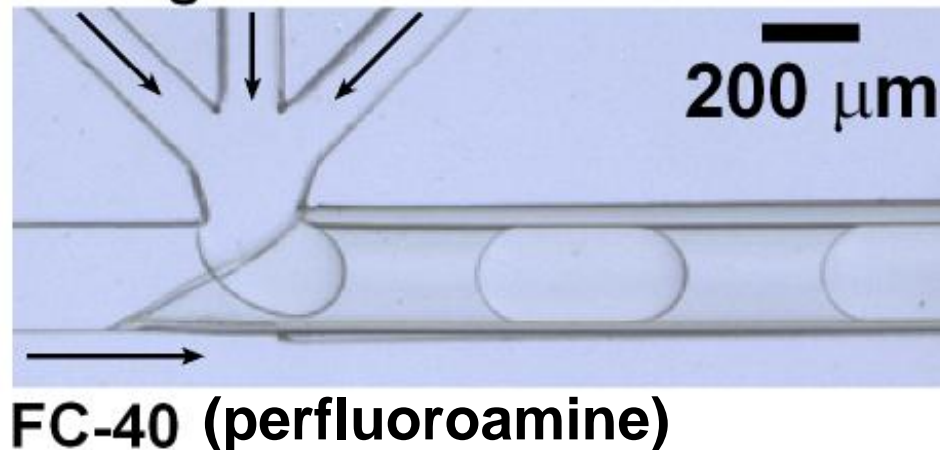
L. Li, D. Mustafi, Q. Fu, V. Tereshko, D.L. Chen, J.D. Tice, R.F. Ismagilov
PNAS, 2006, 103, 19243.

Crystallization of Membrane Proteins using Hybrid Method: Two Technical Developments Alleviate the Challenges

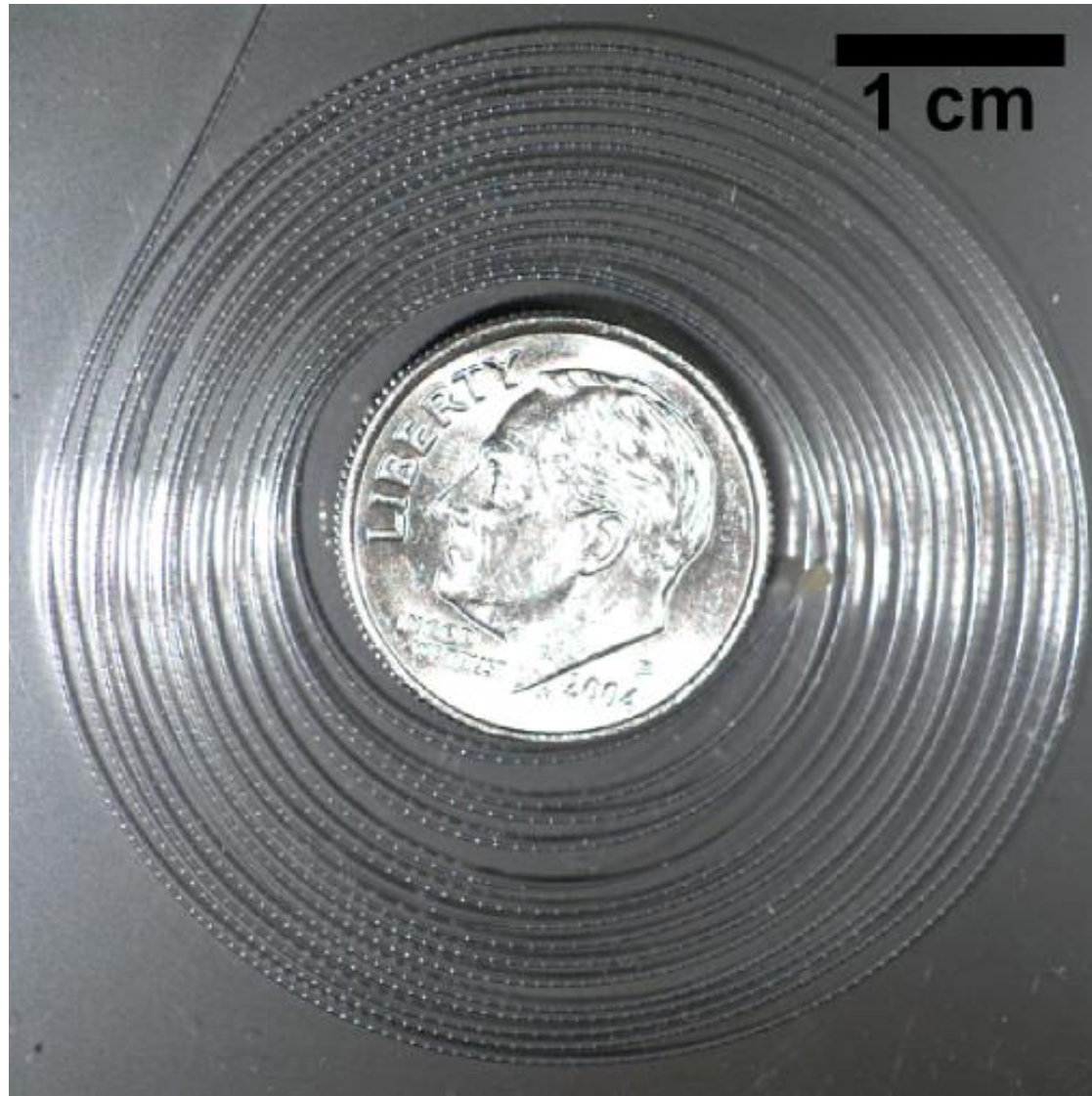
1. The use of **Teflon capillaries** for the formation, transport, and storage of plugs.



2. The use of **perfluoroamines** as carrier fluids
Detergent solution

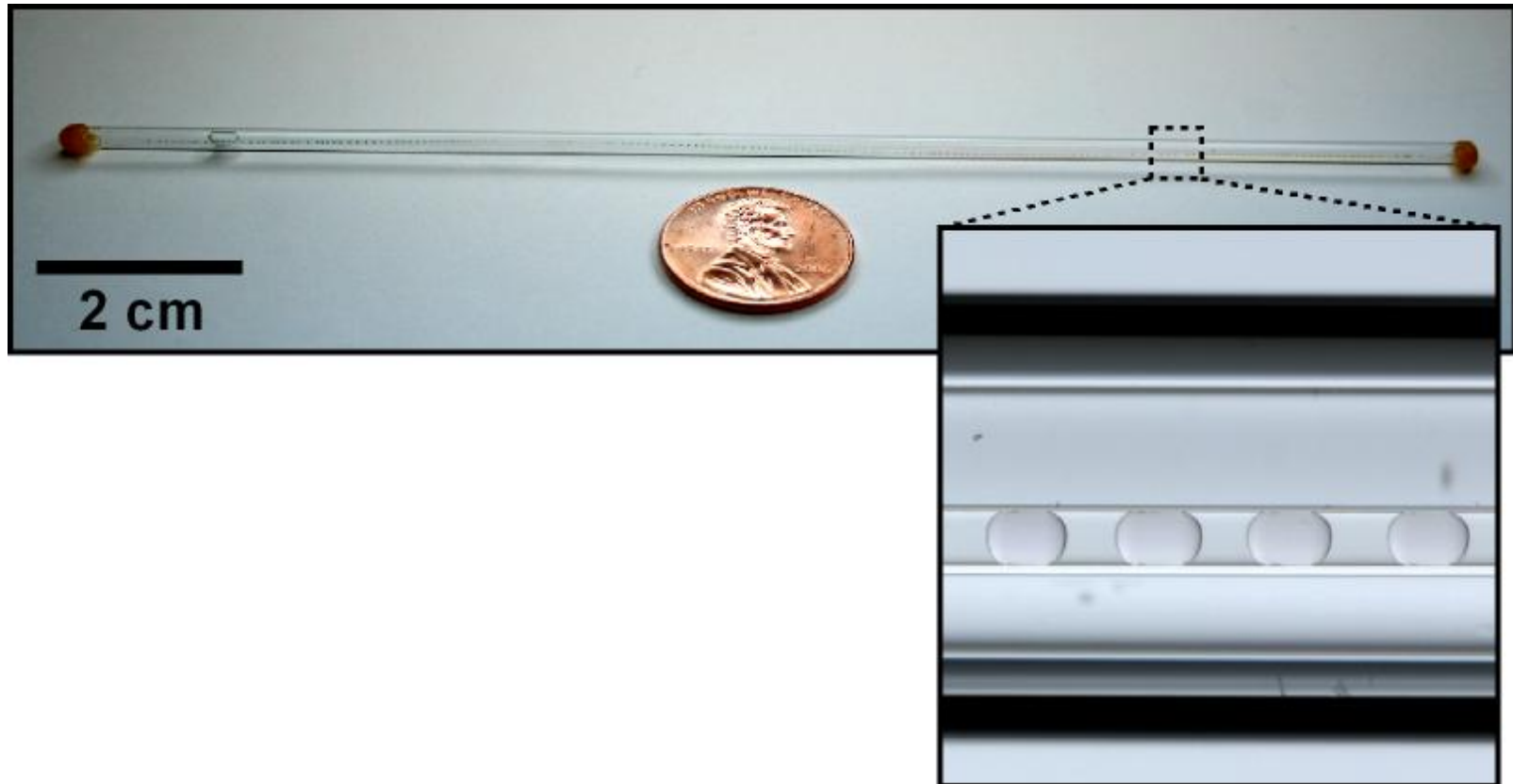
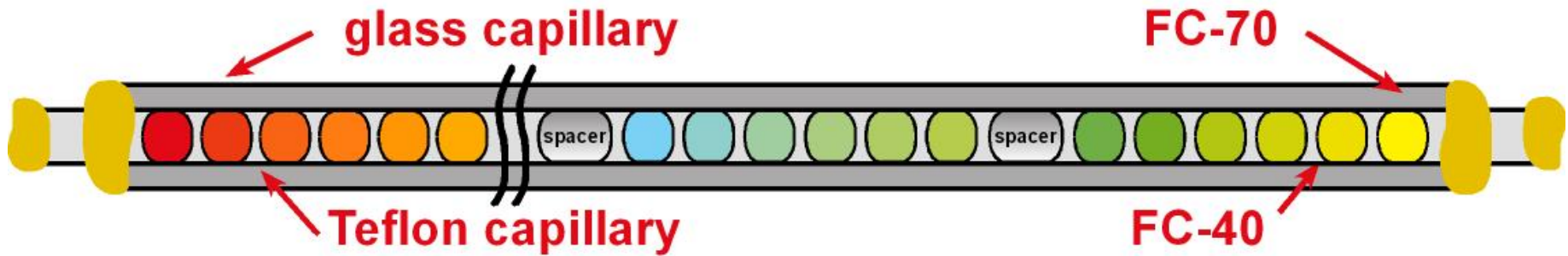


Membrane Protein Crystallization in Teflon Tubing: Compact Plug Storage



1 meter of tubing, ~1000 trials

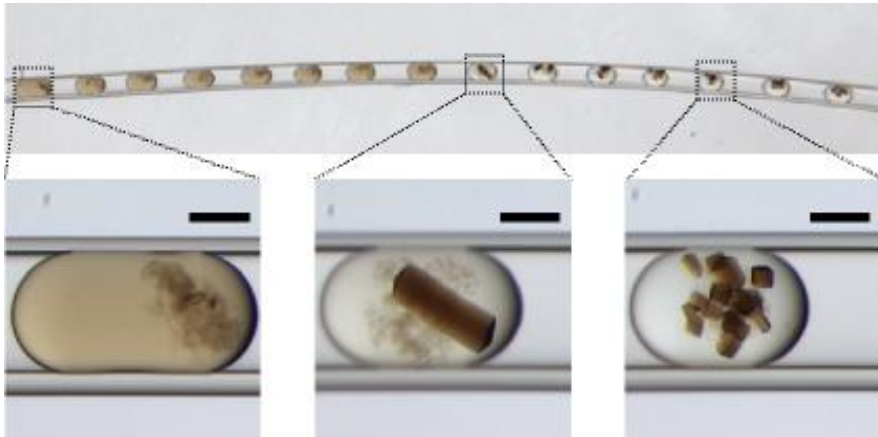
Crystallization of Membrane Proteins using Hybrid Method: Long Term Plug Storage



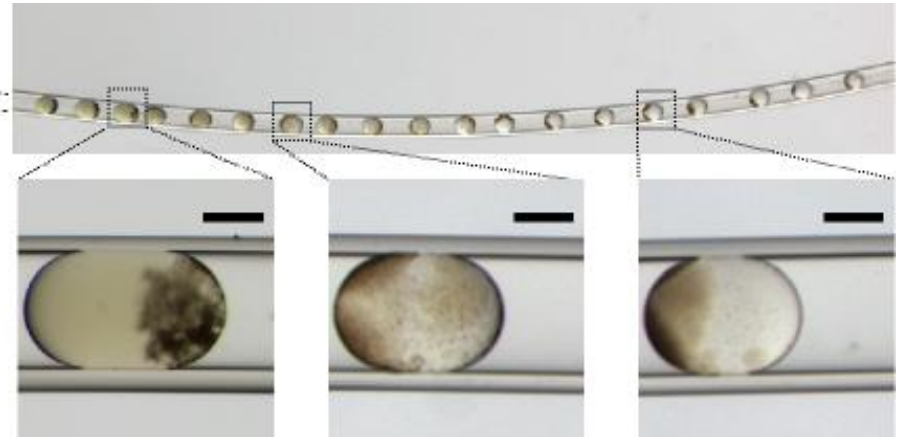
Crystallization of Model Membrane Proteins using Hybrid Method

Reaction Center

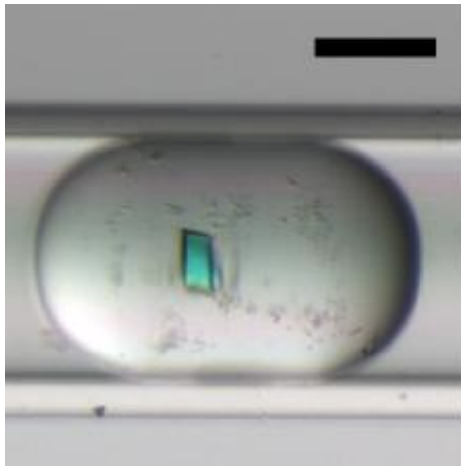
Precipitant #1



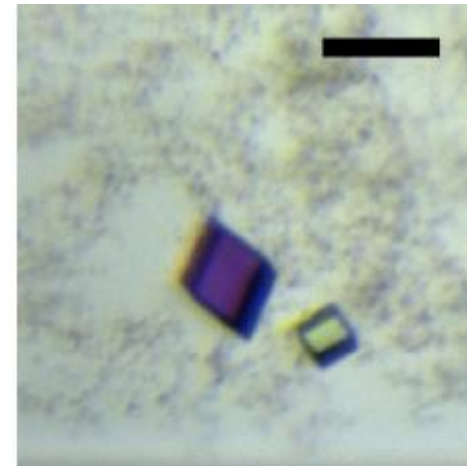
Precipitant #2



Porin

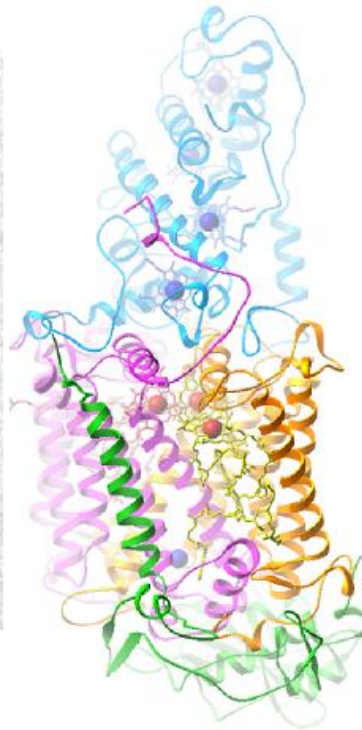
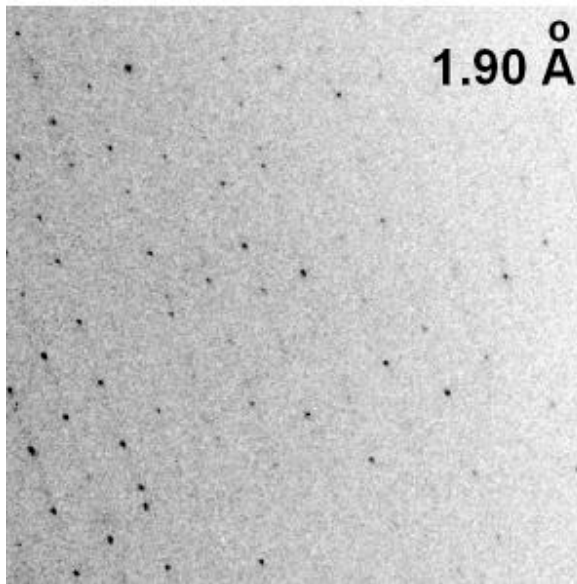


scale up
→

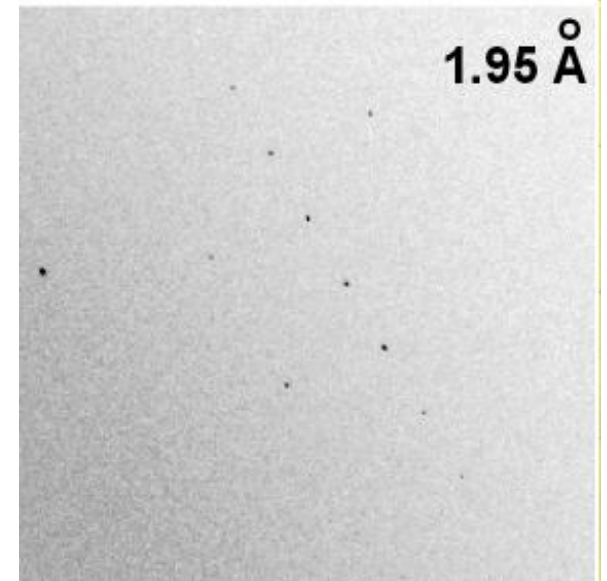


Diffraction of Membrane Protein Crystals Grown in the Hybrid Method

**Reaction Center
(*B. Viridis*)**



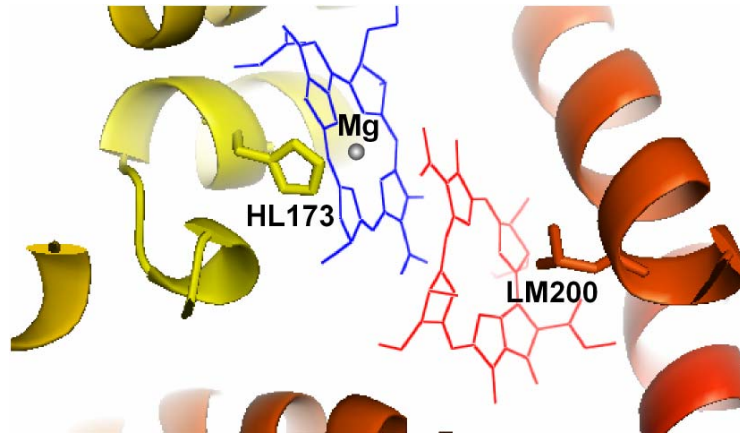
**Porin (*R. Capsulatus*)
in situ diffraction image**



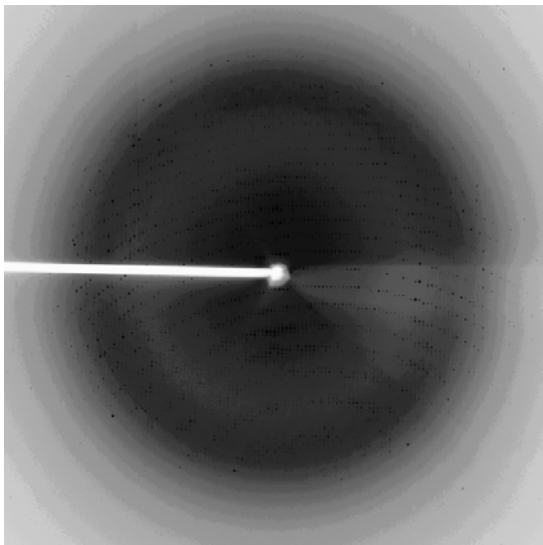
**L. Li, D. Mustafi, Q. Fu, V. Tereshko, D.L. Chen, J.D. Tice, R.F. Ismagilov
PNAS, 2006, 103, 19243.**

Solving New Structures: A Continuous Endeavor

RC Mutant (*B. Viridis*)
Solved at 2.5 Å

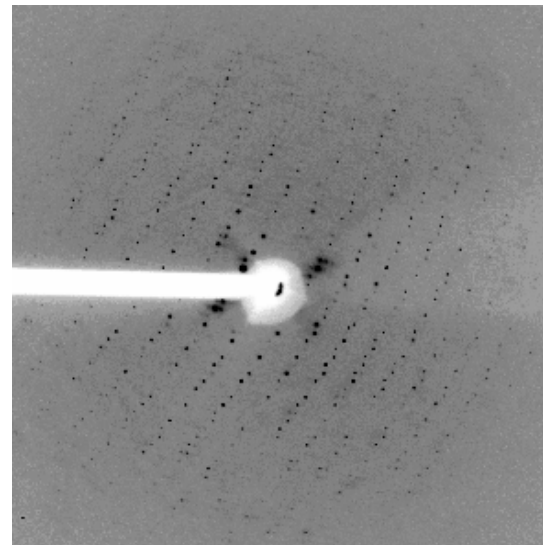


Target 1:



P4
2.9 Å
 $\alpha = \beta = \gamma = 90^\circ$,
 $a = 183.9 \text{ Å}$,
 $b = 183.9 \text{ Å}$,
 $c = 113.9 \text{ Å}$.

Target 2:



P2
6.5 Å
 $\alpha = \gamma = 90^\circ$,
 $\beta = 101.5^\circ$,
 $a = 171.3 \text{ Å}$,
 $b = 232.7 \text{ Å}$,
 $c = 331.7 \text{ Å}$.

Unpublished

Acknowledgements: Ismagilov Group at Chicago

Hemostasis: Christian Kastrup,
Matthew Runyon, Feng Shen,
Rebecca Pompano

Drosophila Development:

Elena Lucchetta, David Adamson

Autocatalytic networks: Cory Gerdt

Collaborators:

James Norris, Nina
Ponomarenko, Philip Laible,
Amy Rosenzweig, James Barber,
Lance Stewart

Protein Crystallization and Droplets:

Liang Li, Cory Gerdt, Delai Chen, Qiang Fu, Debarshi
Mustafi

Microgram organic reactions: Delai Chen, Jason Kreutz

Other Stories: James Boedicker, Meghan Bush

Postdoctoral fellowships, publications: ismagilovlab.uchicago.edu

Financial support:

- NIH/NIBIB
- NIH/NIGMS
- NIH/NCRR (PSI2)
- NSF CAREER
- NSF CRC
- Office of Naval Research,
- Searle Scholars Program,
- Research Corporation,
- Camille and Henry Dreyfus Foundation,
- NSF/Chicago MRSEC,
- DuPont,
- A. P. Sloan,
- Burroughs Wellcome Fund
- Beckman Foundation